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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:10:25 ; Search time 33.5 seconds
(without alignments)
871.180 Million cell updates/sec

Title: US-10-084-507B-22
Perfect score: 1809
Sequence: 1 MGSLSYSEVLPNPKVQEHYNY.....LERGMHPTPTFLEGNVTW 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1809 | 100.0 | 353 | 2 | US-09-582-200A-6 |
| 3 | 1809 | 100.0 | 353 | 2 | US-09-582-200A-12 |
| 4 | 1809 | 100.0 | 353 | 2 | US-09-731-030A-19 |
| 5 | 1803 | 99.7 | 353 | 2 | US-09-582-200A-2 |
| 6 | 1803 | 99.7 | 353 | 2 | US-09-582-200A-5 |
| 7 | 1803 | 99.7 | 353 | 2 | US-09-582-200A-10 |
| 8 | 1760 | 97.3 | 353 | 2 | US-09-274-752D-3 |
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| 11 | 1625.5 | 89.9 | 352 | 2 | US-09-582-200A-11 |
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| 28 | 769 | 42.5 | 378 | 2 | US-09-546-117-2 | Sequence 2, Appli |
| 29 | 769 | 42.5 | 378 | 2 | US-09-169-205D-22 | Sequence 22, Appl |
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| 34 | 535 | 29.6 | 384 | 2 | US-09-731-030A-11 | Sequence 11, Appl |
| 35 | 531 | 29.4 | 384 | 2 | US-09-731-030A-13 | Sequence 13, Appl |
| 36 | 523 | 28.9 | 384 | 2 | US-08-852-824-4 | Sequence 4, Appli |
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| 38 | 515 | 28.5 | 393 | 4 | PCT-US96-10618-3 | Sequence 3, Appli |
| 39 | 512 | 28.3 | 364 | 2 | US-09-169-205D-20 | Sequence 20, Appl |
| 40 | 511 | 28.2 | 364 | 2 | US-08-763-938-2 | Sequence 2, Appli |
| 41 | 509 | 28.1 | 364 | 4 | PCT-US96-10618-2 | Sequence 2, Appli |
| 42 | 506 | 28.0 | 364 | 2 | US-09-731-030A-15 | Sequence 15, Appl |
| 43 | 506 | 28.0 | 364 | 2 | US-09-811-838-2 | Sequence 2, Appli |
| 44 | 492 | 27.2 | 382 | 2 | US-09-169-205D-23 | Sequence 23, Appl |
| 45 | 492 | 27.2 | 382 | 2 | US-09-274-752D-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-09-582-200A-4
; Sequence 4, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:

; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY R
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-200A-4

Query Match 100.0%; Score 1809; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 8.7e-146; Indels 0; Gaps 0;
Matches 353; Conservative 0; Mismatches 0;

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RESULT 2
US-09-582-200A-6
; Sequence 6, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-200A-6

Query Match 100.0%; Score 1809; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 8.7e-146;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-582-200A-12
; Sequence 12, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human EDG-4 #36
US-09-582-200A-12

Query Match 100.0%; Score 1809; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 8.7e-146;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; CURRENT FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Unknown
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; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-19

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RESULT 5
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; Sequence 2, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CONFLICT
; LOCATION: (272)..(274)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
; FEATURE:
; NAME/KEY: misc_feature
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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US-09-582-200A-2

Query Match      99.7%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 2.8e-145;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
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Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLGASWLLISLVLGGLPILGMNCLGLEACS 180
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Db 241 VFTVCMWLPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
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RESULT 6
US-09-582-200A-5
; Sequence 5, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY R
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CONFLICT
; LOCATION: (272)..(274)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (273)...(273)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
US-09-582-200A-5

Query Match          99.7%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 2.8e-145;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7
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; Sequence 10, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
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; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
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; ORGANISM: human EDG-4 polypeptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (273)...(273)
; OTHER INFORMATION: "Xaa" represents any amino acid
US-09-582-200A-10

Query Match          99.7%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 2.8e-145;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNWCLHLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNWCLHLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMHPTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMHPTSPTFLEGNTVV 353
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QY 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNWCLHLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNWCLHLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMHPTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMHPTSPTFLEGNTVV 353

RESULT 8
US-09-274-752D-3
; Sequence 3, Application US/09274752D
; Patent No. 6812335
; GENERAL INFORMATION:
; APPLICANT: Goetzl, Edward L.
; APPLICANT: An, Songzhu
; TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipids and
; FILE REFERENCE: A-67501/DJB/TAL
; CURRENT APPLICATION NUMBER: US/09/274,752D
; CURRENT FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-274-752D-3

Query Match          97.3%; Score 1760; DB 2; Length 353;
Best Local Similarity 98.0%; Pred. No. 1.3e-141;
Matches 346; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAGIVILCCAIVVENLLVLIIVAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNWCLHLEACS 180
Db 121 GSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNWCLHLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMHPTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMHPTSPTFLEGNTVV 353
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US-08-760-936-2
; Sequence 2, Application US/08760936
; Patent No. 5856443
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,936
; FILING DATE: December 6, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-760-936-2

Query Match 89.9%; Score 1625.5; DB 1; Length 352;
Best Local Similarity 89.5%; Pred. No. 3.3e-130;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLSYSLNPNKQEHYNTKETLETQETTSROVASAFIVLCCAIWENLLVLIAR 60
Db 1 MGGLSYSLNPNKQEHYNTKETLDNQETPSRKVASAFIILCCAIWENLLVLIAR 60

Qy 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAFTLSASV 120
Db 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSAFTLSASV 120

Qy 121 FSLIAIAIERHVAIAKVLGYSDKSCRMALLIGASWLISLVGLGLPILGNWCLHLEACS 180
Db 121 FSLIAIAIERQVAIAKVLGYSDKSCRMMLLIGASWLISLITLGGELPILGNWCLHLEACS 180

Qy 181 TVLPLYAKHYVLCVWTTFISILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTTVIVLG 240
Db 181 TVLPLYAKHYVLCVWTTFISVILLAIVALYVRIYFVVRSSHADVAGPQTLALLKTTVIVLG 240

Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAYHLYFAVSTLNSLNPVIYTWRSRDLRREV 300
Db 241 VFIIICWLPAFSILLDDSTCPVRACPVLYKAYFFAFATLNSLNPVIYTWRSRDLRREV 300

Qy 301 RPLCWRPGVQGRRGGTFPGHLLPLRSSSLERGMWMTSPTELEGNTVV 353
Db 301 RPLLCWRQKGATG-RRGNPGRHLLPLRSSSLERGLHMTSPTELEGNTVV 352

RESULT 11
US-09-582-200A-11
; Sequence 11, Application US/09582200A
; Patent No. 6482609

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```
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 352
; TYPE: PRT
; ORGANISM: rat EDG-4 polypeptide
US-09-582-200A-11

Query Match      89.9%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 3.3e-130;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSEYLNPNKQVEHYNYTKETLEQTTSRQVASAFIVILCCAIWENLLVLIAR 60
Db 1 MGSLYSEYLNPEKQVEHYNYTKETLDMQETSPKVASAFIILCCAIWENLLVLIAR 60

Qy 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLGPILGNCLHLEACS 180
Db 121 FSLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSISLVGLGPILGNCLHLEACS 180

Qy 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240
Db 181 TVLPYAKHYVLCVVTIFSVILLAIVALYVRIYFVVRSSHADVAGPQTLALLKTTVTVLG 240

Qy 241 VFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIIICWLPAPFSLILLDSTCPVRACPVLYKAHYFFAFATLNSLNPVIYTWRSRDLRREVL 300

Qy 301 RPLOCWRPGVGQRRRGTPGHLLPLRSSSSLERGHMPTSPTFLEGNTVV 353
Db 301 RPLLCWRQKGATG-RRGNFGHRLPLRSSSSLERGHMPTSPTFLEGNTVV 352

RESULT 13
US-09-225-024-2
; Sequence 2, Application US/09225024
; Patent No. 6518414
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,024
; FILING DATE: 04-JAN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,936
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/196,989
; FILING DATE: 15-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
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; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 352
; TYPE: PRT
; ORGANISM: rat EDG-4 polypeptide
US-09-582-200A-11

Query Match      89.9%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 3.3e-130;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSEYLNPNKQVEHYNYTKETLEQTTSRQVASAFIVILCCAIWENLLVLIAR 60
Db 1 MGSLYSEYLNPEKQVEHYNYTKETLDMQETSPKVASAFIILCCAIWENLLVLIAR 60

Qy 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLGPILGNCLHLEACS 180
Db 121 FSLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSISLVGLGPILGNCLHLEACS 180

Qy 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240
Db 181 TVLPYAKHYVLCVVTIFSVILLAIVALYVRIYFVVRSSHADVAGPQTLALLKTTVTVLG 240

Qy 241 VFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIIICWLPAPFSLILLDSTCPVRACPVLYKAHYFFAFATLNSLNPVIYTWRSRDLRREVL 300

Qy 301 RPLOCWRPGVGQRRRGTPGHLLPLRSSSSLERGHMPTSPTFLEGNTVV 353
Db 301 RPLLCWRQKGATG-RRGNFGHRLPLRSSSSLERGHMPTSPTFLEGNTVV 352

RESULT 12
US-09-169-205D-24
; Sequence 24, Application US/09169205D
; Patent No. 6485922
; GENERAL INFORMATION:
; APPLICANT: Erikson, James
; APPLICANT: Goddard, J. Graham
; APPLICANT: Kiefer, Michael
; TITLE OF INVENTION: METHODS FOR DETECTING COMPOUNDS WHICH MODULATE THE
; TITLE OF INVENTION: ACTIVITY OF AN LPA RECEPTOR
; FILE REFERENCE: 252/004
; CURRENT APPLICATION NUMBER: US/09/169,205D
; CURRENT FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-225-024-2

Query Match 89.9%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 3.3e-130;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGLSEYLNPNKVOEHYNT-KETLETQSTTSQROVASAFIVILCCAIIVVENLLVLIAR 60
DB 1 MGLSEYLNPNKVOEHYNT-KETLETQSTTSQROVASAFIVILCCAIIVVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120

QY 121 FSLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLHLEACS 180
DB 121 FSLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLHLEACS 180

QY 181 TVLPLAKHYVLCVVTIFSIILLAVVALVRYVVRSSHADMAAPOTLLAKTKVTIVLG 240
DB 181 TVLPLAKHYVLCVVTIFSIILLAVVALVRYVVRSSHADMAAPOTLLAKTKVTIVLG 240

QY 241 VFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREYL 300
DB 241 VFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREYL 300

QY 301 RPLQWRPGVGVQRRGTGTPGHLLPLRSSSLERGMPTSPFLEGNVV 353
DB 301 RPLQWRPGVGVQRRGTGTPGHLLPLRSSSLERGMPTSPFLEGNVV 353

RESULT 14
US-09-262-477-2
Sequence 2, Application US/09262477A
Patent No. 6423508
GENERAL INFORMATION:
APPLICANT: George Livi
APPLICANT: Derk Bergema
APPLICANT: Jeffrey Stadel
APPLICANT: Winnie Chan
APPLICANT: Randall Johnson
APPLICANT: Shelagh Wilson
APPLICANT: Jon Chambers
APPLICANT: Phillippe Robert
APPLICANT: Naesirah Khandoudi
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDE SEQUENCES OF HUMAN EDG-1C AND
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND ANTAGONISTS FOR HUMAN
TITLE OF INVENTION: EDG-1C RECEPTOR AND SPHINGOSINE 1-PHOSPHATE LIGAND AND
TITLE OF INVENTION: INTERACTION THEREOF
FILE REFERENCE: GF50006
CURRENT APPLICATION NUMBER: US/09/262,477A
CURRENT FILING DATE: 1999-03-04
EARLIER APPLICATION NUMBER: 60/077,369
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/087,102
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 382
TYPE: PRT
ORGANISM: Human
US-09-262-477-2

Query Match 46.9%; Score 849; DB 2; Length 382;
Best Local Similarity 50.5%; Pred. No. 3.2e-64;

Matches 159; Conservative 60; Mismatches 84; Indels 12; Gaps 2;

QY 3 SLYSEYLNPNKVOEHYNT-KETLETQSTTSQROVASAFIVILCCAIIVVENLLVLIAR 61
DB 14 SSVSDYVNYDIIVRHNTYTKNLSADKENSIKLTSVVFILCCFIILNIFVLLTIWKT 73

QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 121
DB 74 KKFHRPMYVFIIGNLALS DLLAGVAVTANLLSGATTYKLTTPAQWFLREGSMEVALSASF 133

QY 122 SLLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLHLEACST 181
DB 134 SLLATAIERYITMLKMKLHNGSNFRLLLSACWVLSILGLGLPIMGWNCISALSSCST 193

QY 182 VLPLAKHYVLCVVTIFSIILLAVVALVRYVVRSSHADMAAPOTLLA 230
DB 194 VLPLAKHYVLCVVTIFSIILLAVVALVRYVVRSSHADMAAPOTLLA 230

QY 231 LLKTVTVILGVFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
DB 254 LLKTVTVILGVFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290

QY 291 RSRDLRREYLRLPLOC 305
DB 314 TNKEMRRAPFIRIMSC 328

RESULT 15
US-08-196-989B-4
Sequence 4, Application US/08196989B
Patent No. 5585476
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-196-989B-4

Query Match 46.8%; Score 847; DB 1; Length 383;
Best Local Similarity 48.4%; Pred. No. 4.7e-64;
Matches 167; Conservative 61; Mismatches 103; Indels 14; Gaps 4;

QY 3 SLYSEYLNPNKVOEHYNT-KETLETQSTTSQROVASAFIVILCCAIIVVENLLVLIAR 61

Db 15 SQVSDYGNVDIIIVRHVNTGKLNIGVEKDHGIKLTSVWFILICCLIIILENIFVLLTIWKT 74
Qy 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASVF 121
Db 75 KXFHRPMYYFIGNLALSDLLAGVAYTANLLSGATTYKLTPAQWFLREGSMFVALSASVF 134
Qy 122 SLTAIAIERHVAIAKVLGYGSDKSCRMILLIGASWLLISLVGLPLILGWNCIGHLEACST 181
Db 135 SLTAIAIERYITWLKWLHNGNSRSRFLISACWVISLILGGLFIMGWNCISSLSGCSST 194
Qy 182 VLPLYAKHYVLCVVTIFSIILAVVALYVRIYCVVRS-----SHADMAAPOTLA 230
Db 195 VLPLYKHYVILFCTVFTLLLSIVILYCRISLVTRSRRLTFRKNISKARSSEKSLA 254
Qy 231 LLKTVTVLGVFIVCWLPAFISILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
Db 255 LLKTVIIVLSVFACWAPLFIILLLDVGCKAKTCDILYKAHYFLVLAVLNSGTNPFIYTL 314
Qy 291 RSRDLRREVLRLQOWR-PGVGVQGR-RRGGTPGHLLPLRSSSS 333
Db 315 TNKEMRRAPFIRIISCKCPNGDSAGKFKRPIIPGMFGRSKSDNS 359

Search completed: December 4, 2005, 06:24:24
Job time : 34.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:23:26 ; Search time 6 Seconds
(without alignments)
281.714 Million cell updates/sec

Title: US-10-084-507B-22

Perfect score: 1809
Sequence: 1 MGSLSYSEYLNPKVQEHYNY.....LERGMHPTPTFLEGNTVV 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 506 | 28.0 | 364 | 7 | US-11-067-884-2 |
| 2 | 485 | 26.8 | 351 | 7 | US-11-067-884-4 |
| 3 | 481.5 | 26.6 | 353 | 7 | US-11-067-884-6 |
| 4 | 284 | 15.7 | 360 | 6 | US-10-851-667A-26 |
| 5 | 226.5 | 12.5 | 430 | 6 | US-10-992-577-8 |
| 6 | 215.5 | 11.9 | 432 | 6 | US-10-992-577-2 |
| 7 | 205.5 | 11.4 | 420 | 6 | US-10-992-577-6 |
| 8 | 205.5 | 11.4 | 522 | 6 | US-10-510-018-2 |
| 9 | 202.5 | 11.2 | 417 | 6 | US-10-992-577-44 |
| 10 | 198 | 10.9 | 440 | 6 | US-10-502-893-2 |
| 11 | 184 | 10.2 | 342 | 6 | US-10-980-388-118 |
| 12 | 184 | 10.2 | 419 | 7 | US-11-067-884-8 |
| 13 | 167.5 | 9.3 | 508 | 6 | US-10-980-388-112 |
| 14 | 143 | 7.9 | 415 | 6 | US-10-627-633-2 |
| 15 | 143 | 7.9 | 485 | 6 | US-10-821-234-934 |
| 16 | 138 | 7.6 | 313 | 7 | US-11-095-093-2 |
| 17 | 136 | 7.5 | 409 | 6 | US-10-627-633-4 |
| 18 | 126.5 | 7.0 | 340 | 6 | US-10-980-388-117 |
| 19 | 126.5 | 7.0 | 352 | 6 | US-10-627-633-6 |
| 20 | 125 | 6.9 | 287 | 6 | US-10-980-388-66 |
| 21 | 122 | 6.7 | 352 | 7 | US-11-068-686-20 |
| 22 | 121 | 6.7 | 352 | 7 | US-11-068-686-2 |
| 23 | 118 | 6.5 | 355 | 7 | US-11-068-686-4 |
| 24 | 108.5 | 6.0 | 350 | 6 | US-10-502-145-1 |
| 25 | 106 | 5.9 | 347 | 6 | US-10-131-826A-18 |

Sequence 119, App
Sequence 100, App
Sequence 115, App
Sequence 68, Appl
Sequence 199, App
Sequence 8, Appli
Sequence 402, App
Sequence 950, App
Sequence 63, Appl
Sequence 96, Appl
Sequence 116, App
Sequence 2566, Ap
Sequence 444, App
Sequence 52, Appl
Sequence 374, App
Sequence 378, App
Sequence 201, App
Sequence 3306, Ap
Sequence 7826, Ap
Sequence 412, App

26 105.5 5.8 323 6 US-10-980-388-119
27 103.5 5.7 181 6 US-10-980-388-100
28 100 5.5 337 6 US-10-980-388-115
29 97 5.4 204 6 US-10-980-388-68
30 92.5 5.1 286 6 US-10-858-730-199
31 92 5.1 336 7 US-11-099-691-8
32 89.5 4.9 628 7 US-11-082-389-402
33 88 4.9 486 6 US-10-467-657-950
34 87.5 4.8 313 6 US-10-980-388-63
35 86.5 4.8 358 6 US-10-980-388-96
36 86.5 4.8 389 6 US-10-980-388-116
37 86.5 4.8 431 6 US-10-793-626-2566
38 86 4.8 337 6 US-10-793-626-444
39 84.5 4.7 394 6 US-10-392-234A-52
40 83.5 4.6 205 7 US-11-082-389-374
41 83.5 4.6 205 7 US-11-082-389-378
42 83.5 4.6 301 6 US-10-858-730-201
43 83 4.6 392 6 US-10-793-626-3306
44 82.5 4.6 508 6 US-10-467-657-7826
45 82 4.5 462 7 US-11-082-389-412

ALIGNMENTS

RESULT 1

US-11-067-884-2
; Sequence 2, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Liliom, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-884-2

Query Match 28.0%; Score 506; DB 7; Length 364;
Best Local Similarity 34.6%; Pred. No. 4.8e-36;
Matches 117; Conservative 69; Mismatches 122; Indels 30; Gaps 9;

QY 18 NYNKTETQTTTQTSQVASFIVILCAIVVENLLVLIARNSKHSAMVLFGLNLA 77
Db 34 YNRSGKHLATEWNTVSKLVMGIGITVCIFIMLANLLVMVAIYVNRFRPHPIYLLMANLAA 93
QY 78 SLLAGVAFVANTLLSGSVTLRLTPQWFARFGSAPITLSASFVLSILAIARHVAIAKV 137
Db 94 ADFFAGLAYFYLMFNTGNTNRLTSTVLLRGLDTSLTASVANLLAIARHITVFRM 153
QY 138 KLYGDKSCRMILLIGASWLSISLVLGGLPILGWNCLHLEACSTVLPYAKHYVLCVWT 197

Db 154 QLHTRMSNRVVVWVVIWWTMAIVMGAIPTSVGWNCICDIENCSNMAPLYSDSY-LVFWAI 212
Qy 198 FSIILLAV-VALYVRIYCVVR-----SSHADMAAPQ-----TLALLKTVIVLGVFIVC 245
Db 213 FNLVTFVVMVLYAHIFGVQRTWRMSRHS--SGPRNRDRTMMSLLKTVIVLGAFTIC 270
Qy 246 WLPAFSIIILLDVACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRLRREVLRLPQC 305
Db 271 WTPGLVILLDDVCCP--QCDVLAIEKFPULLAEFNSAWNPIIYSTYRDKMSATFQLICC 328
Qy 306 WRPGVGQRRRGTPGHLLPLRSSSLER-----GMH 339
Db 329 QR-----SENPTGPTSSD----RSASSLHNTILAGVH 357

RESULT 2

US-11-067-884-4
; Sequence 4, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:

; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lilioni, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
; APPLICANT: Nussler, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-884-4

Query Match 26.8%; Score 485; DB 7; Length 351;
Best Local Similarity 35.9%; Pred. No. 2.7e-34;
Matches 117; Conservative 57; Mismatches 134; Indels 18; Gaps 4;

Qy 18 YNNKTELETQETTSRQVASAFIVILCCAIIVVENLLVIAVARNSKFSAMVFLGNLAA 77
Db 17 YNNSGKELSSHWRPKDVVVALGLTVSVILVLLTNLLVIAAASNRFPQPIYLLGNLAA 76
Qy 78 SDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITSASVFSLLAIAIERHVAIAK 137
Db 77 ADLFAVAYFLMFHTGTPRTARLSDEGWFLRQGLDTSLSASVATLLAIAVERHSVMV 136
Qy 138 KLYGSDKSCRMILLIGASWLSLVLGGPLIWNCLHLEACSTVLPYAKHYVLCVVTI 197
Db 137 QLHSLRPRGRVMLTVGVVVAALGGLLPAHSHWCLCALDRCSRMAPLLSRSYLAVALS 196
Qy 198 FSIILLAVVALYVRIYCVVRSSHADMA-----APQTLALKTVTVILGVFTVCWLP 248
Db 197 SLVFLMVAVYTRIFVYVRRVQRMAEHVSCHPRYRTTSLVKTVVILIGAFVVCWTP 256
Qy 249 AFSIILLD-YACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRLRREVLRLPQC-- 305
Db 257 GOVLLDGLGC--EESCNVLAKEYFLLLAENSLVNAAVYSCRDAEMRRTFRLLCCAC 314

Qy 306 ----WRPGVGQRRRGTPGHLLP 327
Db 315 LRQTSRVHYTSSAQGGASTRIMLP 340

RESULT 3

US-11-067-884-6
; Sequence 6, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:

; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Lilioni, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
; APPLICANT: Nussler, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-884-6

Query Match 26.6%; Score 481.5; DB 7; Length 353;
Best Local Similarity 32.2%; Pred. No. 5.3e-34;
Matches 101; Conservative 73; Mismatches 121; Indels 19; Gaps 5;

Qy 9 LNPKNQVQHYNYKTELETQETTSRQVASAFIVILCCA-----IVVENLLVIAVARNS 62
Db 1 MNECHYDKHMDFFYNRST-DTVDDMTGTLVILVLCVGTFFCLFFIFFSNLSLVIAAVIKNR 59
Qy 63 KPHSAMYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITSASVFS 122
Db 60 KHPFPFYLLANLAADFFAGIAYFLMFNTGVPVSKTLTVNRWFLRQGLDSSUTASLTN 119
Qy 123 LLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGPLIWNCLHLEACSTV 182
Db 120 LLVIAVERHSIMRVHSNLTKKRVTLILLVWAIAMGAVPTLGNCLCNISACSSL 179
Qy 183 LPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQT-----LALL 232
Db 180 APIYSRSLVFWTVSNLMFAFLIMVVVYIRIYVYVYKRR-TNVLSPTSGSISRRTPMKLM 238
Qy 233 KTVTVILGVFTVCWLPAPAFSILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRS 292
Db 239 KTVMTVLGAFVVCWTPGLVLLLD-GLNCRQCGQVQVHWRWFLLLALLNSVNPVIYSYKD 297
Qy 293 RDLRREVLRLPQCW 306
Db 298 EDMYGTMKMICCF 311

RESULT 4

US-10-851-667A-26
; Sequence 26, Application US/10851667A
; Publication No. US20050260608A1
; GENERAL INFORMATION:

```

RESULT 5
US-10-992-577-8
; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-992-577-2

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; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-067-884-118

Query Match      10.2%; Score 184; DB 6; Length 342;
Best Local Similarity 22.4%; Pred. No. 5,4e-09;
Matches 64; Conservative 53; Mismatches 103; Indels 66; Gaps 11;

Qy 48 VVENLLVLIIVARNKSFHMYLFGNLAASDLLAGVAVANTLSSGVTLLRTPVQWFA 107
Db 46 VEGNLLVMTSVLHFQKLSPTNFLNLASLACADFLVGVTVMLFSM-----VRTVESCYWF 99

Qy 108 REGSAFITYLS-----ASVFSLLAIAIERHVAIAKVLGSDKSCRM-L-LIGASWL 157
Db 100 --GAKFCTLHSCCDVAFICYSSVHLHCFICIDRIYIVTDPVLVYATKFTVSVSGICISVSWI 157

Qy 158 ISLVGLGLP-----ILGNCLGHLEACSTVLPYAKHYVLCVVTIPSIIILA 204
Db 158 LPLTSGAVFYTVGNDGDEELVSLNLCVG---GQIIV---SQGWLIDFLFFIPTLV 211

Qy 205 VVALYRYICVVR-----SSHADMAAPQTLALKTVTVILGVFIVCWL 247
Db 212 MILYSKIFLIAKQAKIETTSSKVESSESYKIRVAKRERKAAKTLGVTVLAFVISWL 271

Qy 248 PAFSTLLILD----YACPVHSCPI-LYKAHYLFAVSTLNLNPVIY 288
Db 272 PYTVDLIDAPMGFLTPAYIYEICWSAY-----NSAMNPLIY 310
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RESULT 12
US-11-067-884-8
; Sequence 8, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardo, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lilom, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
```

```
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-067-884-8

Query Match      10.2%; Score 184; DB 7; Length 419;
Best Local Similarity 25.2%; Pred. No. 6.7e-09;
Matches 91; Conservative 50; Mismatches 132; Indels 88; Gaps 17;

Qy 37 SAFIVILCAIVVENLLVLIIVARNKSFHMYLFGNLAASDLLAGV---AFVANTLLS 93
Db 85 SAIMIFILFVSFLGNLVCLMVYQKAAMRSAINITLLASLAFADMLLAVLNMPFALVTIL- 143

Qy 94 GSVTLRLTPVQWFAREGSAFITLSA--SVFSLLAIAIERHVAIA-----KVLYGSDKSCR 147
Db 144 ---TTRWIFGKFCFVCSAMFFWLFVIEGVAILLIISIDRFLIIVQRQDKLNPY-----R 194

Qy 148 MLLIGASWLIS-----LVLG-----LPILGNCL-GHLEACSTVLPYAKHYVLCVVT 196
Db 195 AKVLIIVSWATSPCFVAFPLAVGNPDQLIPSRAPQCVFGY-----TTNPGYQAYVILISLI 249

Qy 197 IFSIILLAVV-----ALYVRIY-----CVRSSHADMAAQ-----T 228
Db 250 SFFIPFLVILYSFMGILNLTNRHNAIRHSYEPGICLSQASKLGLMSLQRPQMSIDMGFK 309

Qy 229 LALKTIVTVLGVFIVCWLPAPFSTILLDYACPVHSCPTLYKAHYLFAVST-----INS 281
Db 310 TRAFITLILPAFVIVCWAP-FTTYSLVATFSKH----FYQHNFPELSTWLLMLCYLKS 364

Qy 282 LLNPVIYTWRSR---DURREVLRPLQCWPRGVGVQRRRGGTGPHHLLPLRSSSSLERGM 338
Db 365 ALNPLIYVWRIKKFHDACLDMMPKSKFLPOL-----PGHKRRIRPSAVYVCGE 414

Qy 339 H 339
Db 415 H 415
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RESULT 13
US-10-980-388-112
; Sequence 112, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
```

;; PRIOR APPLICATION NUMBER: 60/184,397
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/184,247
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/188,880
;; PRIOR FILING DATE: 2000-03-13
;; PRIOR APPLICATION NUMBER: 60/217,369
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/217,370
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/218,492
;; PRIOR FILING DATE: 2000-07-20
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 184
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 112
;; LENGTH: 508
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-980-388-112

Query Match 9.3%; Score 167.5; DB 6; Length 508;
Best Local Similarity 24.7%; Pred. No. 2e-07;
Matches 49; Conservative 48; Mismatches 84; Indels 17; Gaps 6;

QY 35 VASAFVILCCAVVENLVLAVARNKPHSAMVYFLGNLAASDLLAGVAFVANTLLSG 94
Db 33 IRSTVLVIFPLAASFVGNVIALVLRKPKQLQVTRNFIENLAVTDLQ-LSLVAPVVAT 91
QY 95 SVTLRLTPVQWFAREQ--SAFITLS-----ASVFSLLAIAIERHVAIAKVKLYGSKSCR 147
Db 92 SV-----PLFWPLNSHFCTALVSLTHLPFASVNTVVVSDRYLSIIHPLSPSKMTQR 146
QY 148 M-LLIGASWLSLVGGPIILGNCLGHLE---ACSTVLPLVYKHYVLCVVTIIFSILL 203
Db 147 RGYLLYGTWIVAILQSTPELYGWGOAFDERNALCSMTWIGASPSVTLISVVSFVIPLEI 206
QY 204 AVVALYVRIYCVVRSSHA 221
Db 207 VMIACSVVFCARROHA 224

RESULT 14
US-10-627-633-2
; Sequence 2, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brennand, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-633-2

Query Match 7.9%; Score 143; DB 6; Length 415;
Best Local Similarity 24.2%; Pred. No. 1.9e-05;
Matches 86; Conservative 55; Mismatches 128; Indels 86; Gaps 19;

QY 4 LYSEYL-----NPNKQVQEHYNTKLETQETTSRQVASAFVILCCAVVENLILV 54
Db 35 LPSQYLMELSEHWSNQTDLHY-----VLKPEVAT---ASIFFGILWLSPISFGNSLV 86

QY 55 LIAVARNKPHSAMVYFLGNLAASDLLAGVAFVANTLLS-----GSVTLRLLTPVQWF 106
Db 87 CLVIHRSRRTOSTTNYFVVSMA CADLLISVASTPPVLLQFTTGRWLTGSATCKV--VRVF 144
QY 107 AREGSAFTLSASVFSLLAIAIERHVAIA-----KVKLYGSKSKRMLLLIGASWLI--S 159
Db 145 -----QYLTGPGQIYVLLSICIDRPYTIYVPLSPKVSREKAKK-----MIAASWIFDAG 193
QY 160 LVLGGLPILGNCLGHLEACSTVLP-----LYAKHYVLCVVTIIFSILL-----AVVALY 209
Db 194 FVTPVLFFYGNWDSH---CNYFLPSSWEGTAYTVIHFLVGVFVIPSVLILFYQVKIKYI 250
QY 210 VRIYCVVRSSHADM--AAPQT--LALIKTVITVILGVFIVCWLPAFASILL-----DYACPV 261
Db 251 WRIGHTDGRVTRTMNIVPTKVIKMFLLNLNLLFLLSWLP-FHYAQLWHPHEQDYK--- 306
QY 262 HSCPILYKAHYLFA-----VSTLNSLLNPVIYTWRSRDLRREV-----LRPLOCWR 307
Db 307 -----KSSLVFTAITWISFSSASKPTLYSIYNANFRGMKETFCSMMKCYR 354

RESULT 15
US-10-821-234-934
; Sequence 934, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PRT_SEQ_genes Version 1.0
; SEQ ID NO 934
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-934

Query Match 7.9%; Score 143; DB 6; Length 485;
Best Local Similarity 22.7%; Pred. No. 2.2e-05;
Matches 64; Conservative 57; Mismatches 121; Indels 40; Gaps 11;

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QY 108 REGSAFIT-----LSASVFSLLAIAIERHVAIAKV-----KLYGSKSKRMLLLIGA 154
Db 232 SELCFVTAAPFCNNYVASILLMTVISIDRFLLAVVYPMQSLSWRTLGRASFTCLAIWALAI 291
QY 155 SWLISLVL--GGPLPILGNCLGHLEACSTVL-----PLYAKHYVLCVVTIIFSILLAVV 206
Db 292 AGWVPLVLEQTIQVPGLN-----ITTCHDVLTNETLLEGYYAYYFSAFSAFFVFPVLIIST 347
QY 207 ALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLGVFIVCWLPAFASILLDDYACPVH--SC 264
Db 348 VCYSIIIRCLSSSAVANRSKSRALFSLAA-VFCFIICFGTGNVLLIAHYFSLHSTYT 406
QY 265 PLYKAHYL-FAVSTLNSLLNPVIYTWRSRDLRREVLPLOC 305
Db 407 EBAYPAYLLCVCVSSISSCIDPLIYYASSECQRYVYSILCC 448

Search completed: December 4, 2005, 06:42:27
Job time : 7 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 06:23:06 ; Search time 115.5 Seconds
(without alignments)
1277.002 Million cell updates/sec

Title: US-10-084-507B-22
Perfect score: 1809
Sequence: 1 MGSLEYLNPNKQVHNY.....LRRGMHPTPTFLRGNTVV 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1809 | 100.0 | 353 | 3 | US-09-731-030A-19 |
| 2 | 1809 | 100.0 | 353 | 4 | US-10-084-507B-22 |
| 3 | 1804 | 99.7 | 353 | 3 | US-09-771-063-2 |
| 4 | 1803 | 99.7 | 353 | 4 | US-10-084-507B-17 |
| 5 | 1787 | 98.8 | 353 | 3 | US-09-842-316-8 |
| 6 | 1787 | 98.8 | 353 | 3 | US-09-971-228-9 |
| 7 | 1787 | 98.8 | 353 | 3 | US-09-904-099-33 |
| 8 | 1787 | 98.8 | 353 | 4 | US-10-225-567A-508 |
| 9 | 1787 | 98.8 | 353 | 4 | US-10-228-762-19 |
| 10 | 1787 | 98.8 | 353 | 4 | US-10-393-870-3 |
| 11 | 1787 | 98.8 | 353 | 4 | US-10-421-828-8 |
| 12 | 1787 | 98.8 | 353 | 4 | US-10-715-117-7 |
| 13 | 1787 | 98.8 | 353 | 5 | US-10-498-848-46 |
| 14 | 1783 | 98.6 | 353 | 3 | US-09-771-063-4 |
| 15 | 1625 | 5 | 89.9 | 352 | 4 |
| 16 | 1432 | 79.2 | 372 | 3 | US-09-904-099-37 |
| 17 | 946 | 52.3 | 269 | 3 | US-09-764-886-47 |
| 18 | 946 | 52.3 | 269 | 3 | US-09-764-886-47 |
| 19 | 946 | 52.3 | 274 | 3 | US-09-764-886-74 |
| 20 | 946 | 52.3 | 274 | 3 | US-09-764-891-5338 |
| 21 | 946 | 52.3 | 274 | 3 | US-09-764-886-74 |
| 22 | 860.5 | 47.6 | 384 | 3 | US-09-904-099-5 |
| 23 | 858.5 | 47.5 | 384 | 3 | US-09-904-099-4 |
| 24 | 858 | 47.4 | 391 | 3 | US-09-904-099-3 |
| 25 | 854.5 | 47.2 | 362 | 3 | US-09-993-844-8 |
| 26 | 854.5 | 47.2 | 362 | 4 | US-10-633-438-65 |
| 27 | 854.5 | 47.2 | 362 | 5 | US-10-901-772-65 |

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| 28 | 854.5 | 47.2 | 362 | 6 | US-11-026-435-8 | Sequence 8, Appli |
| 29 | 849 | 46.9 | 341 | 3 | US-09-971-228-13 | Sequence 13, Appl |
| 30 | 849 | 46.9 | 382 | 3 | US-09-971-228-5 | Sequence 5, Appli |
| 31 | 849 | 46.9 | 382 | 3 | US-09-863-455-2 | Sequence 2, Appli |
| 32 | 849 | 46.9 | 382 | 3 | US-09-759-514-2 | Sequence 2, Appli |
| 33 | 849 | 46.9 | 382 | 3 | US-09-904-099-1 | Sequence 1, Appli |
| 34 | 849 | 46.9 | 382 | 4 | US-10-087-192-786 | Sequence 786, App |
| 35 | 849 | 46.9 | 382 | 4 | US-10-225-567A-237 | Sequence 237, App |
| 36 | 849 | 46.9 | 382 | 4 | US-10-295-027-2 | Sequence 2, Appli |
| 37 | 849 | 46.9 | 382 | 4 | US-10-429-160-72 | Sequence 72, Appl |
| 38 | 849 | 46.9 | 382 | 4 | US-10-211-462-2 | Sequence 2, Appli |
| 39 | 849 | 46.9 | 382 | 5 | US-10-491-545A-30 | Sequence 30, Appl |
| 40 | 849 | 46.9 | 382 | 5 | US-10-498-848-38 | Sequence 38, Appl |
| 41 | 849 | 46.9 | 448 | 4 | US-10-425-114-55760 | Sequence 55760, A |
| 42 | 848 | 46.9 | 346 | 3 | US-09-971-228-15 | Sequence 15, Appl |
| 43 | 847 | 46.8 | 383 | 6 | US-11-100-593-8 | Sequence 8, Appli |
| 44 | 845 | 46.7 | 382 | 3 | US-09-969-711-2 | Sequence 2, Appli |
| 45 | 845 | 46.7 | 382 | 4 | US-10-087-192-783 | Sequence 783, App |

ALIGNMENTS

RESULT 1

US-09-731-030A-19
; Sequence 19, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731, 030A
; PRIOR FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-19

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| Query Match | 100.0% | Score | 1809; | DB 3; | Length | 353; | |
| Best Local Similarity | 100.0% | Pred. No. | 3.4e-156; | | | | |
| Matches | 353; | Conservative | 0; | Mismatches | 0; | Gaps | 0; |
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| y | 1 | MGSLEYLNPNKQVHNYTKETLETQTTT | SROVASAFIVILCCAIIVENLLVLI | AVAR | 60 | | |
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Db 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSLRGMHMTSPTFLEGNVTW 353

RESULT 2
US-10-084-507B-22
; Sequence 22, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH
; APPLICANT: VIJAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084,507B
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-507B-22

Query Match 100.0%; Score 1809; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 3.4e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGSLYSEYLNPNKQEHYNTKETLETTTSRQVASAFIVILCCAIIVENLLVLIAR 60
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Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNCLGLEACS 180
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RESULT 3
US-09-771-063-2
; Sequence 2, Application US/09771063
; Patent No. US20010034331A1
; GENERAL INFORMATION:
; APPLICANT: Derk J. Bergsma
; APPLICANT: Nabil Bishourbagy
; APPLICANT: Pamela Lane
; APPLICANT: Xiaotong Li
; APPLICANT: Jeffrey L. Mooney
```

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; APPLICANT: Ping Tsui
; TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
; FILE REFERENCE: GP-70431-C1
; CURRENT APPLICATION NUMBER: US/09/771.063
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/150,650
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/082,776
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-771-063-2

Query Match 99.7%; Score 1804; DB 3; Length 353;
Best Local Similarity 99.4%; Pred. No. 9.7e-156;
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Db 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPIILGNCLGLEACS 180
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Db 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTTVIVLG 240
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Db 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSLRGMHMTSPTFLEGNVTW 353

RESULT 4
US-10-084-507B-17
; Sequence 17, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH
; APPLICANT: VIJAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084,507B
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 353
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; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (273)
; OTHER INFORMATION: Leu or Phe
US-10-084-507B-17

Query Match 99.7%; Score 1803; DB 4; Length 353;
Best Local Similarity 99.4%; Pred. No. 1.2e-155; Mismatches 1; Indels 0; Gaps 0;
Matches 351; Conservative

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Db 1 MGSLSYSEYLNPNKQVQEHYNTKETLETTTSRQVASFIVILCCAIIVVENLLVLIASV 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
QY 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
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Db 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGMHMTSPTFLEGNTVV 353

RESULT 5
US-09-842-316-8
; Sequence 8, Application US/09842316
; Patent No. US20020099191A1
; GENERAL INFORMATION:
; APPLICANT: GASTENHUBER, Johann
; APPLICANT: KOSTENSIS, Eva
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
; FILE REFERENCE: 38005-147
; CURRENT APPLICATION NUMBER: US/09/842,316
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: EP 116589.3
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: EP 108858.2
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 353
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-842-316-8

Query Match 98.8%; Score 1787; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154; Mismatches 3; Indels 0; Gaps 0;
Matches 349; Conservative

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Db 1 MGSLSYSEYLNPNKQVQEHYNTKETLETTTSRQVASFIVILCCAIIVVENLLVLIASV 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
QY 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGMHMTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGMHMTSPTFLEGNTVV 353

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RESULT 7
US-09-904-099-33
; Sequence 33, Application US/09904099
; Publication No. US20030119092A1
; GENERAL INFORMATION:
; APPLICANT: Shankar, Geetha
; APPLICANT: Munning, Jason N
; APPLICANT: Spencer, Juliet V
; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 10602-013-999
; CURRENT APPLICATION NUMBER: US/09/904,099
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-099-33

Query Match      98.8%; Score 1787; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
Db      1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

Qy      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy      121 FSLLAIAIERHVAIAKVLYGSDKSCRMLLLTIGASWLSISLVGLPILGNWCLGLEACS 180
Db      121 FSLLAIAIERHVAIAKVLYGSDKSCRMLLLTIGASWLSISLVGLPILGNWCLGLEACS 180

Qy      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

Qy      241 VFIVCWLPAFSLDLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db      241 VFIVCWLPAFSLDLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy      301 RPLQCMRPGVGQGRRRGTPGHLLPLRSSSSLERGMHMTSPTFLEGNITVV 353
Db      301 RPLQCMRPGVGQGRRRGTPGHLLPLRSSSSLERGMHMTSPTFLEGNITVV 353

RESULT 8
US-10-225-567A-508
; Sequence 508, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 508
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-508

Query Match      98.8%; Score 1787; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
Db      1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

Qy      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy      121 FSLLAIAIERHVAIAKVLYGSDKSCRMLLLTIGASWLSISLVGLPILGNWCLGLEACS 180
Db      121 FSLLAIAIERHVAIAKVLYGSDKSCRMLLLTIGASWLSISLVGLPILGNWCLGLEACS 180

Qy      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

Qy      241 VFIVCWLPAFSLDLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db      241 VFIVCWLPAFSLDLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy      301 RPLQCMRPGVGQGRRRGTPGHLLPLRSSSSLERGMHMTSPTFLEGNITVV 353
Db      301 RPLQCMRPGVGQGRRRGTPGHLLPLRSSSSLERGMHMTSPTFLEGNITVV 353

RESULT 9
US-10-228-762-19
; Sequence 19, Application US/10228762
; Publication No. US20030130493A1
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Huang, Ling Yan
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Salton, John A.
; APPLICANT: Wilson, Amy
; APPLICANT: Nagorny, Raisa
; TITLE OF INVENTION: DNA Encoding Edg7 Receptor
; FILE REFERENCE: 58230-a
; CURRENT APPLICATION NUMBER: US/10/228,762
; CURRENT FILING DATE: 2002-08-26
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: US/09/356,315
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.0 - beta
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-228-762-19

Query Match      98.8%; Score 1787; DB 4; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
Db      1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

Qy      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy      121 FSLLAIAIERHVAIAKVLYGSDKSCRMLLLTIGASWLSISLVGLPILGNWCLGLEACS 180
Db      121 FSLLAIAIERHVAIAKVLYGSDKSCRMLLLTIGASWLSISLVGLPILGNWCLGLEACS 180

Qy      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

Qy      241 VFIVCWLPAFSLDLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db      241 VFIVCWLPAFSLDLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy      301 RPLQCMRPGVGQGRRRGTPGHLLPLRSSSSLERGMHMTSPTFLEGNITVV 353
Db      301 RPLQCMRPGVGQGRRRGTPGHLLPLRSSSSLERGMHMTSPTFLEGNITVV 353
```



QY 181 TVPLVYKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVIVLG 240
Db 181 TVPLVYKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVIVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKHYLFAVSTLNSLLNPVIYVWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKHYLFAVSTLNSLLNPVIYVWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTV 353
Db 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTV 353

RESULT 10

US-10-393-870-3
; Sequence 3, Application US/10393870
; Publication No. US20030219808A1
; GENERAL INFORMATION:
; APPLICANT: KOZIAN, Detlef
; APPLICANT: KOSTENIS, Evi
; APPLICANT: SIEGGER, Karl-Ernet
; APPLICANT: JACOBS, Martina
; APPLICANT: RICARD, Sylvain
; APPLICANT: MACE, Sandrine
; APPLICANT: DELEUZE, Jean-Francois
; TITLE OF INVENTION: ASSOCIATION OF EDG5 POLYMORPHISM WITH TYPE II DIABETES MELLITUS,
; TITLE OF INVENTION: VENOUS THROMBOSIS OR PULMONARY EMBOLISM AND THE USE THEREOF
; FILE REFERENCE: DEAV002/0019 US NP
; CURRENT APPLICATION NUMBER: 2003-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-870-3

Query Match 98.8%; Score 1787; DB 4; Length 353;

Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLETTQTSRQVASAFIVILCCAIVVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLETTQTSRQVASAFIVILCCAIVVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLISLVLGGLPILGWNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLISLVLGGLPILGWNCLGLEACS 180
QY 181 TVPLVYKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVIVLG 240
Db 181 TVPLVYKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVIVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKHYLFAVSTLNSLLNPVIYVWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKHYLFAVSTLNSLLNPVIYVWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTV 353
Db 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTV 353

RESULT 11

US-10-421-828-8
; Sequence 8, Application US/10421828
; Publication No. US20030219874A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIS, Evi

; APPLICANT: GASENHUBER, Johann
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
; FILE REFERENCE: 38005-147
; CURRENT APPLICATION NUMBER: US/10/421,828
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: EP 116589.3
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: EP 108858.2
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-421-828-8

Query Match 98.8%; Score 1787; DB 4; Length 353;

Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLETTQTSRQVASAFIVILCCAIVVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLETTQTSRQVASAFIVILCCAIVVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLISLVLGGLPILGWNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLISLVLGGLPILGWNCLGLEACS 180
QY 181 TVPLVYKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVIVLG 240
Db 181 TVPLVYKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVIVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKHYLFAVSTLNSLLNPVIYVWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKHYLFAVSTLNSLLNPVIYVWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTV 353
Db 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTV 353

RESULT 12

US-10-715-117-7
; Sequence 7, Application US/10715117
; Publication No. US20040171037A1
; GENERAL INFORMATION:
; APPLICANT: LI, JING
; APPLICANT: POWERS, SCOTT
; APPLICANT: SIN, WUN CHEY
; APPLICANT: YANG, JIANXIN
; TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
; FILE REFERENCE: 38002-0062
; CURRENT APPLICATION NUMBER: US/10/715,117
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: 60/427,202
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/434,434
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-117-7

Query Match 98.8%; Score 1787; DB 4; Length 353;

Best Local Similarity 98.9%; Pred. No. 3.4e-154;

| Matches | 349; | Conservative | 1; | Mismatches | 3; | Indels | 0; | Gaps | 0; |
|---------|------|----------------------------------------------------------|-------|------------|----|--------|----|------|----|
| Qy | 1 | MGSLYSYLNPKNVQEHYNTKETELETTSRQVASFIVILCCAIWENLLVLI | AVAR | 60 | | | | | |
| Db | 1 | MGSLYSYLNPKNVQEHYNTKETELETTSRQVASFIVILCCAIWENLLVLI | AVAR | 60 | | | | | |
| Qy | 61 | NSKPHSAMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTT | LSASV | 120 | | | | | |
| Db | 61 | NSKPHSAMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTT | LSASV | 120 | | | | | |
| Qy | 121 | FSLLAIAIERHVAITAKVLYGSDKSCRMILLIGASWLISLVGLGPILGWNCILGH | EACS | 180 | | | | | |
| Db | 121 | FSLLAIAIERHVAITAKVLYGSDKSCRMILLIGASWLISLVGLGPILGWNCILGH | EACS | 180 | | | | | |
| Qy | 181 | TVLPYAKHYVLCVWTTFISILLAVALVYRIYCVRRSSHADMAAPOTALLKTVTV | VLG | 240 | | | | | |
| Db | 181 | TVLPYAKHYVLCVWTTFISILLAVALVYRIYCVRRSSHADMAAPOTALLKTVTV | VLG | 240 | | | | | |
| Qy | 241 | VFIVCWLPAPFSILLDDYACPVHSCPIILYKAHYLFAVSTLNSLNPVIYTWRSRDL | RREVL | 300 | | | | | |
| Db | 241 | VFIVCWLPAPFSILLDDYACPVHSCPIILYKAHYLFAVSTLNSLNPVIYTWRSRDL | RREVL | 300 | | | | | |
| Qy | 301 | RPLQCRWPGVQVQRRGGTPGHILLPLRGSSSSLERGMHPTSTPFLGNTTV | 353 | | | | | | |
| Db | 301 | RPLQCRWPGVQVQRRGGTPGHILLPLRGSSSSLERGMHPTSTPFLGNTTV | 353 | | | | | | |

```

RESULT 13
US-10-498-848-46
; Sequence 46, Application US/10498848
; Publication No. US20050153289A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Method of Analyzing Gene Expression
; FILE REFERENCE: P02-0155PCT
; CURRENT APPLICATION NUMBER: US/10/498,848
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: JP 2001-382053
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: JP 2002-45104
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: JP 2002-140111
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: JP 2002-333769
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 46
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human
US-10-498-848-46

```

| Query Match | 98.8%; | Score 1787; | DB 5; | Length 353; |
|-----------------------|-----------------|---------------------------------------------------------------|-----------|-------------|
| Best Local Similarity | 98.9%; | Pred. No. 3.4e-154; | | |
| Matches 349; | Conservative 1; | Mismatches 3; | Indels 0; | Gaps 0; |
| QY | 1 | MGSLYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVLCCAIWENLLVIAVAR | 60 | |
| DB | 1 | MGSLYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVLCCAIWENLLVIAVAR | 60 | |
| QY | 61 | NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTTLASV | 120 | |
| DB | 61 | NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTTLASV | 120 | |
| QY | 121 | FSLLATAIERHVAIAKYKLXGSDKSCRMILLIGASWLSISLVGLGPIILGWNCGLHLEACS | 180 | |
| DB | 121 | FSLLATAIERHVAIAKYKLXGSDKSCRMILLIGASWLSISLVGLGPIILGWNCGLHLEACS | 180 | |
| QY | 181 | TVIPLYAKHYVLCVVTFISILLAVVALYVRIYCVWRSSHADMAAPQTLALKKTVTIVLG | 240 | |
| DB | 181 | TVIPLYAKHYVLCVVTFISILLAVVALYVRIYCVWRSSHADMAAPQTLALKKTVTIVLG | 240 | |
| QY | 241 | VFIVCMLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVYTYWRSDRLRRREV | 300 | |

| | | | | | | | | |
|----|-----|----------|---------|--------|--------------|---------------|----------|---------------|
| Db | 241 | VFIVCWLP | AFSILLD | YACVH | SCPIYKAHYFAV | STLNSLNPVIYTW | SRDLRREV | 300 |
| Qy | 301 | RPLQCRWP | GVGVQGR | RGTPGH | HLPLR | SSSLERGMH | MPTSP | TFLEGNTVV 353 |
| Db | 301 | RPLQCRWP | GVGVQGR | RRVGT | PGHLLP | LRSSSLERGMH | MPTSP | TFLEGNTVV 353 |

```

RESULT 14
US-09-771-063-4
; Sequence 4, Application US/09771063
; Patent No. US20010034331A1
; GENERAL INFORMATION:
; APPLICANT: Derk J. Bergsma
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Pamela Lane
; APPLICANT: Xiaotong Li
; APPLICANT: Jeffrey L. Mooney
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
; FILE REFERENCE: GP-70431-C1
; CURRENT APPLICATION NUMBER: US/09/771,063
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/150,650
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/082,776
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-771-063-4

```

| Query Match | 98.6% | Score 1783; | DB 3; | Length 353; | |
|-----------------------|-----------------|-----------------------|-------------------------------------|---------------------------|---------------|
| Best Local Similarity | 98.6%; | Pred. No. 8e-154; | | | |
| Matches 348; | Conservative 1; | Mismatches 4; | Indels 0; | Gaps 0; | |
| QY | 1 | MGSLXSEYLNPNKVQEHYNTK | LETQETTSRQVASAFIVILCCAIWENLLVLI | AVAR 60 | |
| DB | 1 | MGGLXSEYLNPNKVQEHYNTK | LETQETTSRQVASAFIVILCCAIWENLLVLI | AVAR 60 | |
| QY | 61 | NSXPHSAMYLFLGNLAASD | LLAGVAFVANTLLSGSVTLRLTPQWFAREGSAF | ITLSASV 120 | |
| DB | 61 | NSXPHSAMYLFLGNLAASD | LLAGVAFVANTLLSGSVTLRLTPQWFAREGSAF | ITLSASV 120 | |
| QY | 121 | FSLLATAIERHVAIAKV | LYGSKRCMMLLIGASWLSISVLGGLPLIGNCLGH | LEACS 180 | |
| DB | 121 | FSLLATAIERHVAIAKV | LYGSKRCMMLLIGASWLSISVLGGLPLIGNWNLGH | LEACS 180 | |
| QY | 181 | TVLPYKAKHYVL | CVVTIFSIILLAVALYVRIYCVVRSSHADMAAP | TALLKTTVTIVLG 240 | |
| DB | 181 | TVLPYKAKHYVL | CVVTIFSIILLAVALYVRIYCVVRSSHADMAAP | TALLKTTVTIVLG 240 | |
| QY | 241 | VFTVCWLP | PAFSILLDYACPVHSCPIYK | AHYLFVNSTLSLNPVITYWRSRDLR | REVL 300 |
| DB | 241 | VFTVCWLP | PAFSILLDYACPVHSCPIYK | AHYLFVNSTLSLNPVITYWRSRDLR | REVL 300 |
| QY | 301 | RPLQCRWPGVGVQGR | RRGGTTPGHLLPLR | SSSLERGMHMTPTSP | TFLEGNTVV 353 |
| DB | 301 | RPLQCRWPGVGVQGR | RRGGTTPGHLLPLR | SSSLERGMHMTPTSP | TFLEGNTVV 353 |

RESULT 15
US-10-084-507B-21
; Sequence 21, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEHS

APPLICANT: VYAS, TEJAL B.
APPLICANT: GUPTA, ASHWANI K.
TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
FILE REFERENCE: 108074-00023
CURRENT APPLICATION NUMBER: US/10/084,507B
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/222,995
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/109,885
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/080,610
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/070,185
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 352
TYPE: PRT
ORGANISM: Rattus sp.
US-10-084-507B-21

Query Match 89.9%; Score 1625.5; DB 4; Length 352;
Best Local Similarity 89.5%; Pred. No. 1.8e-139;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

| | | | |
|----|-----|-----------------------------------------------------------|-----|
| QY | 1 | MGSLYSEYLNPNKQVQEHYNTKETLETOETTSROVASAFIVILCCCAIVVENLLVLI | 60 |
| DB | 1 | MGGLYSEYLNPEKQVQEHYNTKETLDMQETPSRKVASAFIILCCCAIVVENLLVLI | 60 |
| QY | 61 | NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAF | 120 |
| DB | 61 | NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSTPLQWFAREGSAF | 120 |
| QY | 121 | PSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSIVLGGPLPILGWNCL | 180 |
| DB | 121 | PSLLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSILILGGLPILGWNCL | 180 |
| QY | 181 | TVLPLYAKHYVLCVWTIFSIILLAVVALYVRYCVVRSADMAAPQTLALKTV | 240 |
| DB | 181 | TVLPLYAKHYVLCVWTIFSVILLAIVALYVRYFVVRSSHADVAGPQTLALKTV | 240 |
| QY | 241 | VFTVCWLPAPFILLIDYACPVHSCPLYKAHYLFAVSTLNSLNPVIYTWRSRDL | 300 |
| DB | 241 | VFTIICWLPAPFILLIDSTCPVRACPVLYKAHYFAFATLNSLNPVIYTWRSRDL | 300 |
| QY | 301 | RPLQCWRPGVGQRRGGTGGHLLPLRSSSLERGMHMTSPTFLEGN | 353 |
| DB | 301 | RPLLCWRQKGATG-RRGNGPGRHLLPLRSSSLERGLHMTSPTFLEGN | 352 |

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Job time : 116.5 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:38:02 ; Search time 152 seconds
(without alignments)
1638.497 Million cell updates/sec

Title: US-10-084-507B-22

Perfect score: 1809

Sequence: 1 MGSLYSEVLNPNKQVHYNY.....LERGMHMTPTPTFLEGNVTW 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------------|--------------------|
| 1 | 1804 | 99.7 | 353 | 1 EDG5 HUMAN | Q95136 homo sapien |
| 2 | 1631.5 | 90.2 | 352 | 2 EDG3Q7_MOUSE | Q8C3Q7 m mus muscu |
| 3 | 1625.5 | 89.9 | 352 | 1 EDG5 RAT | P47752 rattus norv |
| 4 | 1625.5 | 89.9 | 352 | 2 Q54A16 RAT | Q54A16 rattus norv |
| 5 | 1622.5 | 89.7 | 352 | 1 EDG5 MOUSE | P52592 mus musculu |
| 6 | 998 | 55.2 | 370 | 1 EDG5 BRARE | Q918K8 brachydanio |
| 7 | 932 | 51.5 | 202 | 2 Q91XR0 CAVPO | Q91XR0 cavia porce |
| 8 | 869 | 48.0 | 190 | 2 Q9ESK0 RAT | Q9ESK0 rattus norv |
| 9 | 856 | 47.3 | 382 | 2 Q5R7A1_PONPY | Q5R7A1 pongo pygma |
| 10 | 849 | 46.9 | 382 | 2 Q9NYN8 HUMAN | Q9NYN8 homo sapien |
| 11 | 847 | 46.8 | 383 | 1 EDG1 RAT | P48303 rattus norv |
| 12 | 847 | 46.8 | 383 | 2 Q4V7F6 RAT | Q4V7F6 rattus norv |
| 13 | 845 | 46.7 | 382 | 2 Q9DC35_MOUSE | Q9DC35 m mus muscu |
| 14 | 844 | 46.7 | 382 | 2 Q5B1P0_BOVIN | Q5B1P0 bos taurus |
| 15 | 841 | 46.5 | 373 | 2 Q4T9E2_TETNG | Q4T9E2 tetraodon n |
| 16 | 839 | 46.4 | 382 | 1 EDG1 MOUSE | O08530 mus musculu |
| 17 | 837 | 46.3 | 375 | 2 Q5U389 BRARE | Q5U389 brachydanio |
| 18 | 837 | 46.3 | 382 | 2 Q5E9P3_BOVIN | Q5E9P3 bos taurus |
| 19 | 836.5 | 46.2 | 381 | 1 EDG1 HUMAN | P21453 homo sapien |
| 20 | 835 | 46.2 | 374 | 2 Q6GLJ6_XENLA | Q6GLJ6 xenopus lae |
| 21 | 822.5 | 45.5 | 326 | 2 Q99NR8_CASCN | Q99NR8 castor cana |
| 22 | 820.5 | 45.4 | 325 | 2 Q71BN5_OTOGA | Q71BN5 otleumur ga |
| 23 | 819 | 45.3 | 325 | 2 Q9BF55_ARTJA | Q9BF55 artibeus ja |
| 24 | 817 | 45.2 | 362 | 1 EDG1 BRARE | Q9DDK4 brachydanio |
| 25 | 816.5 | 45.1 | 326 | 2 Q6JC76_9EUTH | Q6JC76 solenodon p |
| 26 | 816.5 | 45.1 | 326 | 2 Q9BF73_CONCR | Q9BF73 condylura c |
| 27 | 816.5 | 45.1 | 326 | 2 Q99NR0_9HYST | Q99NR0 cavia tschu |
| 28 | 816.5 | 45.1 | 326 | 2 Q99NR4_HYSTR | Q99NR4 hystrix bra |
| 29 | 816 | 45.1 | 326 | 2 Q8MK87_TADBR | Q8MK87 tadaria br |
| 30 | 815.5 | 45.1 | 326 | 2 Q99NQ7_AGOTA | Q99NQ7 agouti tacz |
| 31 | 814 | 45.0 | 326 | 2 Q99NR1_HETGA | Q99NR1 heteroceph |

| | | | | | |
|----|-------|------|-----|----------------|--------------------|
| 32 | 813.5 | 45.0 | 326 | 2 Q9BF72 SORAR | Q9BF72 sorex arane |
| 33 | 813.5 | 45.0 | 326 | 2 Q99NQ9_HVDHY | Q99NQ9 hydrochoeru |
| 34 | 812.5 | 44.9 | 326 | 2 Q9BF75_MYRTR | Q9BF75 myrmecophag |
| 35 | 812.5 | 44.9 | 326 | 2 Q9BF76_TAMTE | Q9BF76 tamandua te |
| 36 | 812.5 | 44.9 | 326 | 2 Q99NR3_EREDO | Q99NR3 erethizon d |
| 37 | 811.5 | 44.9 | 326 | 2 Q9BF74_ERICO | Q9BF74 erinaceus c |
| 38 | 811.5 | 44.9 | 326 | 2 Q9BF79_CHOHO | Q9BF79 choleopus h |
| 39 | 811.5 | 44.9 | 326 | 2 Q99NR5_MOUSE | Q99NR5 mus musculu |
| 40 | 811 | 44.8 | 292 | 2 Q91XR2_CAVPO | Q91XR2 cavia porce |
| 41 | 809.5 | 44.7 | 325 | 2 Q99NR9_TAMST | Q99NR9 tamias stri |
| 42 | 807.5 | 44.6 | 326 | 2 Q8MK86_MEGLY | Q8MK86 megaderma l |
| 43 | 807.5 | 44.6 | 326 | 2 Q9BF66_ELERU | Q9BF66 elephantulu |
| 44 | 806.5 | 44.6 | 326 | 2 Q9BF65_ORYAF | Q9BF65 orycteropus |
| 45 | 805.5 | 44.5 | 325 | 2 Q9BF41_PANON | Q9BF41 panthera on |

ALIGNMENTS

RESULT 1
EDG5_HUMAN
ID EDG5_HUMAN STANDARD; PRT; 353 AA.
AC Q95136; Q86UN8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (SLP receptor Edg-5)
DE (Endothelial differentiation G-protein coupled receptor 5)
DE (Sphingosine 1-phosphate receptor 2) (S1P2).
GN Name=EDG5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;
RX PubMed=10617617; DOI=10.1074/jbc.275.1.288;
RA An S., Zheng Y., Bleu T.;
RT "Sphingosine 1-phosphate-induced cell proliferation, survival, and
RT related signaling events mediated by G protein-coupled receptors Edg3
RT and Edg5.";
RL J. Biol. Chem. 275:288-296(2000).
RL [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.
RL [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.J., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -|- FUNCTION: Receptor for the lysophospholipid sphingosine 1-phosphate (S1P). S1P is a bioactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues. When expressed in rat HTC4 hepatoma cells, is capable of mediating S1P-induced cell proliferation and suppression of apoptosis.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC -|- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC -----

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CC -----

DR EMBL; AF034780; AAC98919.1; -; mRNA.

DR EMBL; AY262688; AAP20652.1; -; Genomic_DNA.

DR EMBL; BC069598; AAH69598.1; -; mRNA.

DR Ensembl; ENSG00000175898; Homo sapiens.

DR HGNC; HGNC:3169; EDG5.

DR MIM; 605111; -.

DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.

DR GO; GO:0008289; F:lipid binding; TAS.

DR GO; GO:0000187; P:activation of MAPK; TAS.

DR GO; GO:0000187; P:activation of MAPK; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.

DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

DR InterPro; IPR004063; EDG5_receptor.

DR InterPro; IPR000276; GPCR_Rhodspn.

DR InterPro; IPR004061; S1P_receptor.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR01525; EDG5RECEPTOR.

DR PRINTS; PR00237; GPCRHOOPS.

DR PRINTS; PR01523; S1PRECEPTOR.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Glycoprotein; Lipoprotein;

KW Multigene family; Palmitate; Receptor; Transducer; Transmembrane.

FT TOPO_DOM 1 34 Extracellular (Potential).

FT TRANSMEM 35 59 1 (Potential).

FT TOPO_DOM 60 66 Cytoplasmic (Potential).

FT TRANSMEM 67 95 2 (Potential).

FT TOPO_DOM 96 109 Extracellular (Potential).

FT TRANSMEM 110 128 3 (Potential).

FT TOPO_DOM 129 147 Cytoplasmic (Potential).

FT TRANSMEM 148 173 4 (Potential).

FT TOPO_DOM 174 189 Extracellular (Potential).

FT TRANSMEM 190 210 5 (Potential).

FT TOPO_DOM 211 233 Cytoplasmic (Potential).

FT TRANSMEM 234 255 6 (Potential).

FT TOPO_DOM 256 271 Extracellular (Potential).

FT TRANSMEM 272 292 7 (Potential).

FT TOPO_DOM 293 353 Cytoplasmic (Potential).

FT LIPID S-palmitoyl cysteine (By similarity).

FT CARBOHYD 19 19 N-linked (GlcNAc. .) (Potential).

FT CONFLICT 113 113 F -> S (in Ref. 1).

FT CONFLICT 318 318 G -> V (in Ref. 1).

SQ SEQUENCE 353 AA; 38867 MW; 8E37084284ABF7E8 CRC64;

Query Match 99.7%; Score 1804; DB 1; Length 353;

Best Local Similarity 99.4%; Pred. No. 4.7e-114;

Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLSYEVLPNPKVQEHYNYTKETLETQETTSRQVASAFIVLCAIVVNLVLIASV 60

Db |||||

QY 61 NSKFHSMYLFIGNLAASDLGAVFVANTLLSGSVTLRLTPVQVFAREGSAFILTASV 120

Db |||||

QY 61 NSKFHSMYLFIGNLAASDLGAVFVANTLLSGSVTLRLTPVQVFAREGSAFILTASV 120

Db |||||

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLITGASWLSLVLGGLPILGWNCLGLEACS 180

Db |||||

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLITGASWLSLVLGGLPILGWNCLGLEACS 180

Db |||||

QY 181 TVLPYAKHYVLCVVTTFISILLAVVALYVRIYCVVSSHADMAAPOTLALKTKVTIVLG 240

Db |||||

QY 181 TVLPYAKHYVLCVVTTFISILLAVVALYVRIYCVVSSHADMAAPOTLALKTKVTIVLG 240

Db |||||

QY 241 VFIVCWLPAFISILLDDYACPVHSCPIYKAYHLPFAVSTLNSLNPVIYTWRSRDLRREVL 300

Db |||||

QY 241 VFIVCWLPAFISILLDDYACPVHSCPIYKAYHLPFAVSTLNSLNPVIYTWRSRDLRREVL 300

Db |||||

QY 301 RPLQWRPGVGQRRRGSTPGHLLPLRSSSSSLERGMHMTPTFTFLEGNTVW 353

Db |||||

QY 301 RPLQWRPGVGQRRRGSTPGHLLPLRSSSSSLERGMHMTPTFTFLEGNTVW 353

Db |||||

RESULT 2

Q8C3Q7 MOUSE PRELIMINARY; PRT; 352 AA.

AC Q8C3Q7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430039A03 product:endothelial differentiation, sphingolipid G-protein-coupled receptor, 5, full insert sequence (Endothelial differentiation, sphingolipid G-protein-coupled receptor, 5).

DE Name=Edg5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RT Carnici P., Hayashizaki Y.;

RL "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Harsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;

| | |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|
| DR | Pfam, PF00001; 7tm_1; 1. |
| DR | PRINTS; PRO1525; EDGSRCEPTOR. |
| DR | PRINTS; PRO0237; GPCRRHODOPN. |
| DR | PRINTS; PRO1523; S1PRECEPTOR. |
| DR | PROSITE; PS0262; G PROTEIN RECP F1.2; 1. |
| KW | G-protein coupled receptor; Receptor; Transducer; Transmembrane. |
| SQ | SEQUENCE 352 AA; 39829 MW; 6A3E426B0FE54406 CRC64; |
| Query Match 90.2%; Score 1631.5; DB 2; Length 352; Best Local Similarity 90.1%; Pred. No. 2.1e-102; Matches 318; Conservative 13; Mismatches 21; Indels 1; Gaps 1; | |
| QY | 1 MGSLSEYLNPKNKQBHYNYTKETLETTOETTSSQVASFIVILCCAIVVENLLVLIAVAR 60 |
| DB | 1 MGGLSEYLNPKEVLSEHYNTKETLDMQETTSKKVASAFIIICCAIVVENLLVLIAVAR 60 |
| QY | 61 NSKFHSAMYLFLGNLAASDLLAGAVFANTLLSGSVTLRLTPQWFAREGSAFITLSASV 120 |
| DB | 61 NSKFHSAMYLFLGNLAASDLLAGAVFANTLLSHVTLSLTPQWFAREGSAFITLSASV 120 |
| QY | 121 FSLLAIAIERHVAIAKVLYGSDKSCRMLLIGASWMLISLVGGPLPILGWNCILGLEACS 180 |
| DB | 121 FSLLAIAIERQVALAKVLYGSDKSCRMMLIGASWMLISLILGGPLPILGWNCILGLEACS 180 |
| QY | 181 TVLPYAKHYVLCVWTIFSIILLANVALYRIYCVVRSSHADMAAPOTLLAKTIVTVLG 240 |
| DB | 181 TVLPYAKHYVLCVWTIFSIVLLAIVALYRIYFVVRSHADVAGPQTALLKTIVTVLG 240 |
| QY | 241 VFTVCWLPAFSILLDVPCHVSPCILYKAHYLFVASTNLNLNPVIYTWRSRDLRREV 300 |
| DB | 241 VFIIICWLPFAFSILLIDSTCFPRACPVLYKAHYFFATNLNLNPVIYTWRSRDLRREV 300 |
| QY | 301 RPLQCWRPGVGQGRRGCTPGHHLLPLRSSSSLERGMHMTPTPTFLEGNVTV 353 |
| DB | 301 RPLQCWRPGKGVGTG-RRGGNPGHRLLPLRSSSSLERGMHMTPTPTFLEGNTVV 352 |
| RESULT 3 EDG5 RAT STANDARD; PRT; 352 AA. ID AC EDG5 RAT STANDARD; PRT; 352 AA. DC PA7752; DT 01-FEB-1996 (Rel. 33, Created) DT 01-FEB-1996 (Rel. 33, Last sequence update) DT DT 10-MAY-2005 (Rel. 47, Last annotation update) DE D Spingosine 1-phosphate receptor Edg-5 (SIP receptor Edg-5) (G-protein DE coupled receptor H218) (AGR16) (Endothelial differentiation G-protein DE coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2). DN Name=Edg5; OS Rattus norvegicus (Rat). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muroidae; Muridae; Murinae; Rattus. OX NCBI_TaxID=10116; RN [1] RP NUCLEOTIDE SEQUENCE. RC TISSUE=Brain, and Lung; RC MEDLINE=94373324; PubMed=8087418; DOI=10.1006/mcne.1994.1024; RX MacLennan A.J., Browe C.S., Gaskin A.A., Lado D.C., Shaw G.; RT "Cloning and characterization of a putative G-protein coupled receptor potentially involved in development"; RL Mol. Cell. Neurosci. 5:201-209(1994). RN [2] RP NUCLEOTIDE SEQUENCE. RC TISSUE=Aortic smooth muscle; RX MEDLINE=93176155; PubMed=8382486; RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M., RA Takawa Y.; RT "Molecular cloning of a novel putative G protein-coupled receptor expressed in the cardiovascular system." RL Biochem. Biophys. Res. Commun. 190:1104-1109(1993). RN [3] RP NUCLEOTIDE SEQUENCE. RC TISSUE=Brain; | |

RX MEDLINE=98072391; PubMed=9409733; DOI=10.1016/S0014-5793(97)01301-X;
RA An S., Bleu T., Huang W., Hallmark O.G., Coughlin S.R., Goetzl E.J.;
RT "Identification of cDNAs encoding two G protein-coupled receptors for
RL lysophospholipids.";
RL FEBS Lett. 417:279-282 (1997).
RN [4]
RP PHARMACOLOGICAL CHARACTERIZATION.
RX PubMed=10383399; DOI=10.1074/jbc.274.27.18997;
RA Ancellin N., Hia T.;
RT "Differential pharmacological properties and signal transduction of
RT the sphingosine 1-phosphate receptors EDG-1, EDG-3, and EDG-5.";
RL J. Biol. Chem. 274:18997-19002 (1999).
CC -!- FUNCTION: Receptor for the lysophospholipid sphingosine 1-
CC phosphate (S1P). S1P is a bioactive lysophospholipid that elicits
CC diverse physiological effect on most types of cells and tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in all developing tissues with
CC highest levels detected in primitive, transformed cells. Relative
CC abundance: lung > kidney = skin = gut > spleen > brain > liver.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U10699; AA19241.1; -; mRNA.
DR EMBL; AF022138; AAC53494.1; -; mRNA.
DR PIR; JCI1465; JCI1465.
DR Ensembl; ENSRNOG0000020653; Rattus norvegicus.
DR RGD; 68334; Edg5.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IDA.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; S1P_Receptor.
DR Pfam; PF00001; 7tm_1; 1_1_Receptor.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 34 Extracellular (Potential).
FT TRANSMEM 35 59 1 (Potential).
FT TOPO_DOM 60 66 Cytoplasmic (Potential).
FT TRANSMEM 67 95 2 (Potential).
FT TOPO_DOM 96 109 Extracellular (Potential).
FT TRANSMEM 110 128 3 (Potential).
FT TOPO_DOM 129 147 Cytoplasmic (Potential).
FT TRANSMEM 148 173 4 (Potential).
FT TOPO_DOM 174 189 Extracellular (Potential).
FT TRANSMEM 190 210 5 (Potential).
FT TOPO_DOM 211 233 Cytoplasmic (Potential).
FT TRANSMEM 234 255 6 (Potential).
FT TOPO_DOM 256 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT TOPO_DOM 293 352 Cytoplasmic (Potential).
FT LIPID S-palmitoyl cysteine (By similarity).
FT CARBOHYD 19 19 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 38735 MW; 9C933A18E756CE1E CRC64;

Query Match 89.9%; Score 1625.5; DB 1; Length 352;
Best Local Similarity 89.5%; Pred. No. 5.5e-102;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLSYSLNPNKVOEHNYTKETLETQETTSRQVASFIVILCAIIVENLLVLIIVAR 60
DB 1 MGGLSYSLNPNKVOEHNYTKETLDMQETPSRKVASAFIILCAIIVENLLVLIIVAR 60

QY 61 NSKFHSAWYFLGNIILAAADLLAGVAVFANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
|||||

Db 61 NSKFHSAWYFLGNIILAAADLLAGVAVFANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLIAIAIERHVAIAKVLGSDKSCRMILLIGASWLSISVLGSLPIGLWNCGLHLEACS 180
|||||
Db 121 FSLIAIAIERQVAIAKVLGSDKSCRMMLIGASWLSISLGLPLTIGWNCGLHLEACS 180
|||||
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYRIYCVVRSSHADMAAPOTLALLKTVTVILG 240
|||||
Db 181 TVLPLYAKHYVLCVVTIFSVILLIAVALYRIYFVVRSSHADVAGPOTLALLKTVTVILG 240
|||||
QY 241 VFIVCMLPAPFISILLDYACVPHSCPIYLKAYHLYFAVATLSLNLNPVIYTWRSRLRREVL 300
|||||
Db 241 VFIIICMLPAPFISILLDSTCPVACPVLYKAYHLYFAVATLSLNLNPVIYTWRSRLRREVL 300
|||||
QY 301 RPLQWRPGVGVQRRGGTTPGHHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
|||||
Db 301 RPLLQWRQKGGATG-RRGGNPGHRLPLRSSSSSLERGLHMTPTPTFLEGNTVV 352
|||||
RESULT 4
Q54A16 RAT
ID Q54A16 RAT PRELIMINARY; PRT; 352 AA.
AC Q54A16;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AGR16.
GN Name=AGR16;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
RX MEDLINE=93176155; PubMed=8382486;
RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
RA Takawa Y.;
RT "Molecular cloning of a novel putative G protein-coupled receptor
RT expressed in the cardiovascular system.";
RL Biochem. Biophys. Res. Commun. 190:1104-1109 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
RA Gonda K., Takawa Y.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AB016931; BAA32454.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophingolipid and lysophosphatidic acid . . .; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR004063; EDG5_Receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; S1P_Receptor.
DR Pfam; PF00001; 7tm_1; 1_1_Receptor.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 352 AA; 38735 MW; 9C933A18E756CE1E CRC64;

Query Match 89.9%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 5.5e-102;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLSYSLNPNKVOEHNYTKETLETQETTSRQVASFIVILCAIIVENLLVLIIVAR 60
DB 1 MGGLSYSLNPNKVOEHNYTKETLDMQETPSRKVASAFIILCAIIVENLLVLIIVAR 60

QY 61 NSKFHSAWYFLGNIILAAADLLAGVAVFANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
|||||


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Db 61 NSKFSHMYLFLGNLAASDLLAGVAVFVANTLLSGPVTLSLTPLOWFAREGSAFILTASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGLPILGWNCLEHLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGLPILGWNCLEHLEACS 180
Qy 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTTIVL 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTTIVL 240
Qy 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHLYPAVSTLNSLNPVITWRSRDLRREVL 300
Db 241 VFIIICWLPFAFSLILDSTCPVRACPVLYKAHYFFAFATLNSLNPVITWRSRDLRREVL 300
Qy 301 RPLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGHMPSTPFLGNTVV 353
Db 301 RPLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGHMPSTPFLGNTVV 352

RESULT 5
EDG5_MOUSE
ID EDG5_MOUSE STANDARD; PRT; 352 AA.
AC P52592; Q9R236;
DT 01-OCT-1996 (Rel. 34, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
DE (lysophospholipid receptor B2) (Endothelial differentiation G-protein coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2).
GN Name=Edg5; Synonyms=Gpcr13, Lpb2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RC STRAIN=129/SvJ;
RX MEDLINE=99132320; PubMed=9931453; DOI=10.1016/S0378-1119(98)00589-7;
RA Zhang G., Contos J.J.A., Weiner J.A., Fukushima N., Chun J.;
RT "Comparative analysis of three murine G-protein coupled receptors activated by sphingosine-1-phosphate.";
RL Gene 227:89-99(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 62-241.
RC TISSUE=Testis;
RX MEDLINE=94116980; PubMed=8288218;
RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I., Copeland N.G., Jenkins N.A.;
RT "Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptors.";
RL Genomics 18:175-184(1993).
CC -!- FUNCTION: Receptor for the lysophingolipid sphingosine 1-phosphate (S1P). S1P is a bioactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Most abundant in heart and lung; low, but clearly observed in kidney, liver and thymus; much lower but detectable in brain, testis, stomach and intestine. Not significantly detected in any of the sections of embryonic day (E) 14-18, except in embryonic brain.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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CC EMBL; AF108020; AAD16976.1; -; Genomic_DNA.
CC EMBL; L20334; AAI16846.1; -; mRNA.
CC PIR; E48909; E48909.
CC Ensembl; ENSMUSG00000043895; Mus musculus.
```

```
DR MGI; MGI:99569; Edg5.
DR GO; GO:0007610; P:behavior; IMP.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; S1P_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR0237; GPCRHOODOPSN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; PARTIAL.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 34 Extracellular (Potential).
FT TRANSMEM 35 59 1 (Potential).
FT TOPO_DOM 60 66 Cytoplasmic (Potential).
FT TRANSMEM 67 95 2 (Potential).
FT TOPO_DOM 96 109 Extracellular (Potential).
FT TRANSMEM 110 128 3 (Potential).
FT TOPO_DOM 129 147 Cytoplasmic (Potential).
FT TRANSMEM 148 173 4 (Potential).
FT TOPO_DOM 174 189 Extracellular (Potential).
FT TRANSMEM 190 210 5 (Potential).
FT TOPO_DOM 211 233 Cytoplasmic (Potential).
FT TRANSMEM 234 255 6 (Potential).
FT TOPO_DOM 256 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT TOPO_DOM 293 305 Cytoplasmic (Potential).
FT LIPID 305 305 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 19 19 N-linked (GlcNAc...) (Potential).
FT CONFLICT 166 166 P -> S (in Ref. 2).
FT CONFLICT 175 175 Q -> K (in Ref. 2).
FT CONFLICT 189 189 H -> R (in Ref. 2).
SQ SEQUENCE 352 AA; 38871 MW; 9A3E456DD488FE6B CRC64;

Query Match 89.7%; Score 1622.5; DB 1; Length 352;
Best Local Similarity 89.8%; Pred. No. 8.7e-102;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSELYNPNKQSEHYNYTKETLETQETTSRQVASAFIVILCCAIWVENLLVIAVAR 60
Db 1 MGSLYSELYNPNKQSEHYNYTKETLDMQETTSRQVASAFIVILCCAIWVENLLVIAVAR 60
Qy 61 NSKFSHMYLFLGNLAASDLLAGVAVFVANTLLSGVTLRLTPVQVFAREGSAFILTASV 120
Db 61 NSKFSHMYLFLGNLAASDLLAGVAVFVANTLLSGVTLRLTPVQVFAREGSAFILTASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGLPILGWNCLEHLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGLPILGWNCLEHLEACS 180
Qy 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTTIVL 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTTIVL 240
Qy 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHLYPAVSTLNSLNPVITWRSRDLRREVL 300
Db 241 VFIIICWLPFAFSLILDSTCPVRACPVLYKAHYFFAFATLNSLNPVITWRSRDLRREVL 300
Qy 301 RPLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGHMPSTPFLGNTVV 353
Db 301 RPLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGHMPSTPFLGNTVV 352

RESULT 6
EDG5_BRARE
ID EDG5_BRARE STANDARD; PRT; 370 AA.
AC Q918K8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
DE (Sphingosine 1-phosphate receptor 2) (S1P2).
```

GN Name=edg5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS MIL HIS-150 AND CYS-167.
RX MEDLINE=20365730; PubMed=10910360; DOI=10.1038/35018092;
RA Kupperman E., An S., Osborne N., Waldron S., Stainier D.Y.R.;
RT "A sphingosine-1-phosphate receptor regulates cell migration during
vertebrate heart development.";
RL Nature 406:192-195(2000).
CC -!- FUNCTION: Receptor for the lysosphingolipid sphingosine 1-
phosphate (S1P). S1P receptor is critical for cell migration and
epithelial integrity during vertebrate embryogenesis.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: The expression pattern is complex and
dynamic. Maternal expression is found in a diffuse pattern
throughout the blastoderm, and this pattern persists through the
onset of gastrulation. More pronounced expression can be seen at
tailbud stage in the anterior portion of the embryo and along the
midbrain/hindbrain boundary and the tip of the tail where blisters
later develop in receptor mutants. At the 18-somite stage,
expression appears just lateral to the midline, and as the
myocardial precursors migrate to the midline, their location
overlaps with this domain of receptor expression.
CC -!- DISEASE: Defects in edg5 are a cause of heart development
abnormality named miles apart (mil). In all vertebrates, the
myocardial progenitors involute early during gastrulation and come
to occupy bilateral positions in the anterior lateral plate
mesoderm (lPM). During somitogenesis, these cells undergo a second
phase of migration toward the midline and fuse to form the
definitive heart tube. Defects in EDG5 disrupt this process,
leading to the formation of two laterally positioned hearts
(cardia bifida). The mil phenotype for which two recessive alleles
exist, mil(m93) and mil(te273) are fully penetrant.
CC Phenotype as homozygotes for either single mutant allele. In
addition to cardia bifida, mil mutants display epithelial tail
blisters, indicative of a defect in epithelial integrity.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF260256; AAF88001.1; -, mRNA.
DR Ensembl; ENSDARG0000009719; Danio rerio.
DR ZFIN; ZDB-GENE-020123-2; edg5.
DR InterPro; IPR000987; EDG1receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; S1P_receptor.
DR Pfam; PF00001; 7cm; 1.
DR PRINTS; PR00642; EDG1RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Disease mutation; G-protein coupled receptor; Glycoprotein;
Lipoprotein; Palmitate; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 57 Extracellular (Potential).
FT TRANSMEM 58 78 1 (Potential).
FT TOPO_DOM 79 87 Cytoplasmic (Potential).
FT TOPO_DOM 88 108 2 (Potential).
FT TRANSMEM 109 128 Extracellular (Potential).
FT TOPO_DOM 129 147 3 (Potential).
FT TOPO_DOM 149 167 Cytoplasmic (Potential).
FT TRANSMEM 168 188 4 (Potential).
FT TOPO_DOM 189 214 Extracellular (Potential).

FT TRANSMEM 215 235 5 (Potential).
FT TOPO_DOM 236 254 Cytoplasmic (Potential).
FT TRANSMEM 255 275 6 (Potential).
FT TOPO_DOM 276 289 Extracellular (Potential).
FT TRANSMEM 290 310 7 (Potential).
FT TOPO_DOM 311 370 Cytoplasmic (Potential).
FT LIPID 325 325 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 24 24 N-linked (GlcNAc-) (potential).
FT VARIANT 150 150 R -> H (in mil; allele m93; lack of S1P-mediated signaling).
FT VARIANT 167 167 R -> C (in mil; allele te273; lack of S1P-mediated signaling).
SQ SEQUENCE 370 AA; 41777 MW; 8C6B3A06DEEA6757 CRC64;
Query Match 55.2%; Score 998; DB 1; Length 370;
Best Local Similarity 58.2%; Pred. No. 1.5e-59;
Matches 199; Conservative 52; Mismatches 73; Indels 18; Gaps 4;
QY 3 SLYSEYLNPNKVQSHYNTKE-----TLEOTETT SRQVASAFIVILCCAIVVENLLV 54
DB 17 SKSYQYFNKLIQVHYITAKEMTAEELDRDIESQSLSS--LNILFVVISIILLENLLV 74
QY 55 LIAVARNSKFHSAMYLEFLGNLAASDLLAGVAFVANTLLSGSVTLRLTFVQVFAREGSAFI 114
DB 75 LIAVFRNKKFHSAMFFIGNLAFSDLLAGSAYIANIFLSGPRTHLTPVQVFIREGTAFI 134
QY 115 TLSASVPSLLAIAIERHVAITAKVKLYGSDKSCRMILLIGASWLISLVGLPILGWNCGLG 174
DB 135 ALSASVPSLLAIAIERHVAITAKVKLYGSDKSCRMILLIGASWLISLVGLPILGWNCGLG 194
QY 175 HLEACSVPLIYAKHYVLCVVTIPFSITLLAVVALYVRIYCVRSSSHADMAAPQTALLKT 234
DB 195 NLDDCSAVLPUNTRYIRFVVTIPFSITLLSIVLYVRIYLVIRTSHQEATNSPAYALLKT 254
QY 235 VTIVLGVFVFCWLPFAFSILLIDYACPVHSCPILYKAHYLFAVSTLNSLLNPVITYWRSRD 294
DB 255 VTIVLGVFVFCWLPFAFSILLIDYACPVHSCPILYKAHYLFAVSTLNSLLNPVITYWRSRD 314
QY 295 LRREVLPLQWRPGVGVQRRRGTPGHH-LPLRSSSSLE 335
DB 315 MRKEFLRVLCW-----GLLNCGRPPHRCVMPVKSSSSME 349

RESULT 7

Q91XR0_CAVPO
ID Q91XR0_CAVPO PRELIMINARY; PRT; 202 AA.
AC Q91XR0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endothelial differentiation sphingolipid G-protein-coupled receptor 5 (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=hartley; TISSUE=Myenteric plexus;
RA Segura B.J., Xiao L., Cowles R.A., Turner D.J., Logsdon C.D.,
RA Mulholland M.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289992; AAK83087.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysosphingolipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR004063; EDG5_Receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; S1P_receptor.
DR Pfam; PF00001; 7cm_1; 1.

DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
PT NON_TER 202
SQ SEQUENCE 202 AA; 21836 MW; D9814EC85B42320A CRC64;

Query Match 51.5%; Score 932; DB 2; Length 202;
Best Local Similarity 91.1%; Pred. No. 2.4e-55;
Matches 184; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 20 YKTELTOETTSRQVASAFIVILCAI VVENLLVLI AVARNSKFHSAMYLFLGNLAASD 79
Db 1 YKETLDVRETTSRQVASAFIVILCAI VVENLLVAVGRNSKLHSAWYLFIGNLAASD 60

Qy 80 LLAGVAPVANTLGGSVTLRTLPVQWFAREGS AFITLSASFSLAI AIERHVATAKVKL 139
Db 61 LLAGVAPIANTLGGSVTQLTPVEVFAREGS AFITLSASFSLAI AIERHVATAKVKL 120

Qy 140 YGSDKSCRMILLIGASWISLVGLGPILGWNC LGHLSEACSTVLPL YAKHYVLCVVTTFS 199
Db 121 YGSDKSCRMILLIGASWISLVGLGPILGWNC LGRLDTCS TPLPIYAKQYVLCVVTTFS 180

Qy 200 IILLAVVALYRIYCVRSSHA 221
Db 181 VILLAIVLYRIYCVRSSHA 202

RESULT 8
ID QESKO_RAT PRELIMINARY; PRT; 190 AA.

AC QESKO;
AD QESKO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative G-protein coupled receptor (Fragment).
GN Name=GPCR18;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley/Hsd;
RA Carroll S.L., Miller M.L.; Benedict-Hamilton H.M.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF090995; AAC24359.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004619; F:lysophingolipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPRO04063; EDG5_receptor.
DR InterPro; IPRO00276; GPCR Rhodpsn.
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PROSITE; PS00237; S1PRECEPTOR.
DR PROSITE; PS00262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
PT NON_TER 190
SQ SEQUENCE 190 AA; 20718 MW; 3CA0A5C188E168B1 CRC64;

Query Match 48.0%; Score 869; DB 2; Length 190;
Best Local Similarity 88.4%; Pred. No. 4.1e-51;
Matches 168; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 94 GSUTLTLPVQWFAREGS AFITLSASFSLAI AIERHVATAKVKGSDKCRMLLLIG 15
Db 1 GPVTLSLTLPVQWFAREGS AFITLSASFSLAI AIERHVATAKVKGSDKCRMLLLIG 60

Qy 154 ASWLISLVGLGPILGWNCLGHLEACSTVLPL YAKHYVLCVVTTFSII ILLAVVALYRIY 213
Db 61 ASWLISLVGLGPILGWNCLDHLEACSTVLPL YAKHYVLCVVTFISVILLAI VALYRIY 120

Qy 214 CVVRSSHADMAPOITALTKTVTVILGVFI VCWLPFAFSILLDDYACPVSCHPILYKAHYL 273
Db 121 FVVRSSHADVAGPQTALLTKTVTVILGV FIICWLPFAFSILLDDSTCPVRACPVYKAHYF 180

Qy 274 FAYSTINSLL 283
Db 181 FAFATNLSLL 190

RESULT 9
ID QS7AL_PONPY PRELIMINARY; PRT; 382 AA.

AC QS7AL;
AD QS7AL;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFPz469M119.
GN Name=DKFPz469M119;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German CDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Meves H.W., Weil B., Amid C., Osanger A., Fobbo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; CR60217; CAH92359.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004619; F:lysophingolipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPRO00987; EDG1receptor.
DR InterPro; IPRO02277; EDG2_recepser.
DR InterPro; IPRO00276; GPCR Rhodpsn.
DR InterPro; IPRO04063; S1P Receptor.
DR PANTHER; PTHR19266.SF5; EDG1receptor; 1.
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PR00842; EDG1RECEPTOR.
DR PRINTS; PR01148; EDG2RECEPTOR.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1;
DR PROSITE; PS00262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Hypothetical protein; Receptor;
Transducer; Transmembrane.
SQ SEQUENCE 382 AA; 42773 MW; 6F0841D0E93789CC CRC64;

Query Match 47.3%; Score 856; DB 2; Length 382;
Best Local Similarity 51.1%; Pred. No. 5.9e-50;
Matches 161; Conservative 59; Mismatches 83; Indels 12; Gaps 2;

Qy 3 SLYSLEYLNPNKVQHNYNT-KETLETQETT SRQVASAFIVILCCA IVENLLVIAVARN 61
Db 14 SSVSDYNDYDIIVRHYNVTGKNISAD KENSIKLTSVVFILICCFILENFVLLTIWKT 73

Qy 62 SKFHSMAYLFIGNLAASDLLAGVAFVANTL GGSVTLRTLPVQWFAREGS AFITLSASF 121
Db 74 KKFRHPMYFFIGNALS DLLAGVAYTANLLI SGATTYKLTPAQWFLREGSFALSASF 133

NCBI_TaxID=10116;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TJSUVE=Cerebellum;
RX MEDLINE=95047498; PubMed=7959012; DOI=10.1016/0378-1119(94)90171-6;
RA Lado D.C., Browe C.S., Gaikin A.A., Borden J.M., MacLennan A.J.;
RT "Cloning of the rat edg-1 immediate-early gene: expression pattern
suggests diverse functions.";
RL Gene 149:331-336(1994).
CC -1- FUNCTION: Receptor for the lysophospholipid sphingosine 1-
phosphate (S1P). S1P is a bioactive lysophospholipid that elicits
diverse physiological effect on most types of cells and tissues.
CC This inducible epithelial cell G-protein-coupled receptor may be
involved in the processes that regulate the differentiation of
endothelial cells. Seems to be coupled to the G(i) subclass of
heteromeric G proteins (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DEVELOPMENTAL STAGE: First detected at embryonic day 15. At
postnatal day 14 detected in skin, spleen, liver, kidney, heart,
testicle, lung and brain. At adulthood is most abundant in brain.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; U10303; AAA83418.1; -; mRNA.
CC PR; 153870; I53870.
CC RG; 61958; Edg1.
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO; GO:0045446; P:endothelial cell differentiation; IEP.
CC GO; GO:0030182; P:neuron differentiation; IEP.
CC GO; GO:0019226; P:transmission of nerve impulse; IEP.
CC InterPro; IPR000987; EDG1receptor.
CC InterPro; IPR002277; EDG2 receptor.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR004061; S1P Receptor.
CC PANTHER; PTHR19266.SF5; EDG1receptor; 1.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00642; EDG1RECEPTOR.
CC PRINTS; PR01148; EDG2RECEPTOR.
CC PRINTS; PR00237; GPCRRHODOPSIN.
CC PRINTS; PR01523; SUPRECEPTOR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW phosphorylation; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 47 Extracellular (Potential).
FT TRANSMEM 48 72 1 (Potential).
FT TOPO_DOM 73 79 Cytoplasmic (Potential).
FT TRANSMEM 80 108 2 (Potential).
FT TOPO_DOM 109 122 Extracellular (Potential).
FT TRANSMEM 123 141 3 (Potential).
FT TOPO_DOM 142 160 Cytoplasmic (Potential).
FT TRANSMEM 161 186 4 (Potential).
FT TOPO_DOM 187 202 Extracellular (Potential).
FT TRANSMEM 203 223 5 (Potential).
FT TOPO_DOM 224 257 Cytoplasmic (Potential).
FT TRANSMEM 258 279 6 (Potential).
FT TOPO_DOM 280 295 Extracellular (Potential).
FT TRANSMEM 296 316 7 (Potential).
FT TOPO_DOM 317 383 Cytoplasmic (Potential).
FT MOD_RES 354 354 Phosphoserine (Potential).
FT LIPID 329 329 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 31 31 N-linked [GlcNAc...] (potential).
SQ SEQUENCE 393 AA; 42746 MW; 090BAGAE90DB4F3 CRC64;
Best Local 46.8%; Score 847; DB 1; Length 383;
Query Match Similarity 48.4%; Pred. No. 2.4e-49;
Matches 167; Conservative 61; Mismatches 103; Indels 14; Gaps 4;

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 4, 2005, 06:38:17 ; Search time 24.5 Seconds
(without alignments)
1386.307 Million cell updates/sec

Title: US-10-084-507B-22
Perfect score: 1809
Sequence: 1 MGSLYSEYLNPNKQVQEHYNY.....LGRGMHMTSPTFLEBNTVV 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------|--------------------|
| 1 | 1625.5 | 89.9 | 352 | JC1465 | probable G protein |
| 2 | 847 | 46.8 | 383 | I53870 | Edg-1 orphan recep |
| 3 | 836.5 | 46.2 | 381 | A35300 | G protein-coupled |
| 4 | 817.5 | 45.2 | 362 | JC7559 | sphingosine 1-phos |
| 5 | 808 | 44.7 | 180 | E48909 | G protein-coupled |
| 6 | 769 | 42.5 | 378 | JC5245 | G protein-coupled |
| 7 | 506 | 28.0 | 364 | JC5293 | lysophosphatidic a |
| 8 | 352.5 | 19.5 | 323 | S43850 | melanocortin 3 rec |
| 9 | 348.5 | 19.3 | 360 | B46647 | melanocortin recep |
| 10 | 348 | 19.2 | 362 | I65990 | G protein-coupled |
| 11 | 345 | 19.1 | 330 | A55689 | G protein-coupled |
| 12 | 339.5 | 18.8 | 363 | S48697 | probable G protein |
| 13 | 338.5 | 18.7 | 323 | S36636 | melanocortin recep |
| 14 | 336 | 18.6 | 330 | S40454 | G protein-coupled |
| 15 | 305 | 16.9 | 325 | JC2193 | melanocortin recep |
| 16 | 302 | 16.7 | 372 | I49008 | melanocortin-5 rec |
| 17 | 301.5 | 16.7 | 314 | S71420 | melanocortin 1 rec |
| 18 | 300 | 16.6 | 473 | A33117 | cannabinoid recep |
| 19 | 299.5 | 16.6 | 332 | A57055 | melanocortin recep |
| 20 | 295.5 | 16.3 | 325 | JC5592 | melanocortin 5 rec |
| 21 | 291.5 | 16.1 | 325 | JN0764 | melanocortin recep |
| 22 | 290.5 | 16.1 | 347 | S70364 | cannabinoid recep |
| 23 | 290 | 16.0 | 317 | S45708 | MSH receptor - bov |
| 24 | 288.5 | 15.9 | 314 | S70005 | melanocortin 1 rec |
| 25 | 286 | 15.8 | 472 | S17595 | cannabinoid recep |
| 26 | 285 | 15.8 | 315 | S25581 | melanocyte-stimula |
| 27 | 284.5 | 15.7 | 317 | T12055 | melanocyte stimula |
| 28 | 284.5 | 15.7 | 412 | A48978 | adenosine receptor |
| 29 | 284 | 15.7 | 360 | S36750 | cannabinoid recep |

ALIGNMENTS

RESULT 1

JC1465

probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JC1465

R:Okazaki, H.; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takuwa, Y

Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993

A:Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in t

A:Reference number: JC1465; MUID:93176155; PMID:8382486

A:Accession: JC1465

A:Molecule type: mRNA

A:Residues: 1-352 <OKA>

A:Cross-references: UNIPROT:P47752; UNIPARC:UPI000000007D; GB:AB016931; NID:93445557; PI

A:Experimental source: aortic smooth muscle

C:Superfamily: G protein-coupled receptor edg-1

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:35-59/Domain: transmembrane #status predicted <TM1>

F:67-95/Domain: transmembrane #status predicted <TM2>

F:110-128/Domain: transmembrane #status predicted <TM3>

F:148-173/Domain: transmembrane #status predicted <TM4>

F:190-210/Domain: transmembrane #status predicted <TM5>

F:234-255/Domain: transmembrane #status predicted <TM6>

F:272-293/Domain: transmembrane #status predicted <TM7>

F:19/Binding site: carboxylate (Asn) (covalent) #status predicted

F:142,145,218,219,329,330,331,332/Binding site: phosphate (Ser) (covalent) #status predi

F:313/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 89.9%; Score 1625.5; DB 2; Length 352;

Best Local Similarity 89.5%; Pred No. 6.3e-125;

Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLYSEYLNPNKQVQEHYNYTKETLTETTSRQVASAFIVILCAIVVENLLVIAVAR 60

Db 1 MGGLYSEYLNPNKQVQEHYNYTKETLTQMDETSPKVASAFIILCAIVVENLLVIAVAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGVTLTLTPVQFARGSGAFITLSASV 120

Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGVTLTLTPVQFARGSGAFITLSASV 120

QY 121 FSLLAIAIETRHVAIAKVKLYGSKRMLLIGASWLSLVLGGLPILGNCLGHLEACS 180

Db 121 FSLLAIAIETRHVAIAKVKLYGSKRMLLIGASWLSLVLGGLPILGNCLGHLEACS 180

QY 181 TVLPLYAKHYVLQVVTIFSIILLAVVALYVRIYCVVRRSHADMAAPQTLLAKTKVTIVLG 240

Db 181 TVLPLYAKHYVLQVVTIFSVILLAIAVALYVRIYFVRRSHADVAGPQTLLAKTKVTIVLG 240

QY 241 VFTVCWLPAFSLILLDYACPVHSCBILYKAHYLFAVSTLNSLLNPVIYVTRSRDLRREVL 300

Db 241 VFTICWLPAFSLILLDSTCFVRCPCVLYKAHYFFAFATLNSLLNPVIYVTRSRDLRREVL 300


```

RESULT 8
S43850
melanocortin 3 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jan-1995 #sequence_revision
C:Accession: S43850; S37153
R:Desarnaud, F.; Labbe, O.; Eggerickx, D.; Vassart, G.; Parmentier, M.
27-Jan-1995 #text_change 09-Jul-2004

```


A;Residues: 1-330 <IIS>
A;Cross-references: UNIPROT:P46089; UNIPARC:UPI0000001624; GB:L32830; GB:L32831; NID:g60
R;Eggerickx, D.; Denef, J.F.; Labbe, O.; Hayashi, Y.; Refetoff, S.; Vassart, G.; Parmant
Biochem. J. 309, 837-843, 1995

A;Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutively a
A;Reference number: S58521; MUID:9536960; PMID:7639700

A;Accession: S58521
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-330 <EGG>

A;Cross-references: UNIPARC:UPI0000001624; GB:X83956; NID:g1061125; PIDN:CAA58787.1; PID
R;Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, I
Genomics 23, 609-618, 1994

A;Title: Cloning of human genes encoding novel G protein-coupled receptors.

A;Reference number: A55733; MUID:95154831; PMID:7851889

A;Accession: C55733

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-292 <MAR>

A;Cross-references: UNIPARC:UPI000016A113; GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:

C;Genetics:

A;Gene: GDB:GPR3

A;Cross-references: GDB:371695; OMIM:600241

A;Map position: lp36.1-lp34.3

C;Superfamily: melanocortin receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.1%; Score 345; DB 2; Length 330;
Best Local Similarity 33.3%; Pred. No. 1.1e-20;
Matches 96; Conservative 49; Mismatches 107; Indels 36; Gaps 11;

Qy 38 AFIVILCCA---IVVENLLVLIIVARNKSFHSAMYLFLGNLAASDLLAGVAFV---ANTL 91

Db 42 ANDVVLCSGLTVSCENALVVAIVGTFAFPAPMFLVGSIAVADLLAGLGLVLFHFAVF 101

Qy 92 LSGSVTLRLTPVQWFAREGSAPITLSASVFSLLAIAIERHVAIAKVLYGSDKS-CRMLL 150

Db 102 CIGSAEMLVLV-----GVLAWAFTASIGSLAIVTDVRLSYLNALTYSETTVTRTV 155

Qy 151 LIGASWLSLVLGGLPIGLWNCGLHLEACSTVPLXAKHYVLCVVTIFSI---ILLAVVAL 208

Db 156 MLVMYGALGLGLPLVLANCLDGLTTCGVVYPLSKNHLVLAIAFFMVFGLMLQLYQA 215

Qy 209 YVRIYCVVRSSHADMAAPQTLAL-----LKTVTIVLGVFIVCWLPAFSILLDY 257

Db 216 ICRIVC-----RHAQOIALQRHLHPASHVATKKGATLAVVLGAPAAWLPFTVCLG 271

Qy 258 ACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRLRREVLRLPQC 305

Db 272 A---HS-PPLY-TYLTLLPATYNSMINPIIYAFRNQVQK-VLMAVCC 313

RESULT 12

S48697

probable G protein-coupled receptor protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

A;Accession: S48697

R;Song, Z.H.; Young III, W.S.; Brownstein, M.J.; Bonner, T.I.

FEBS Lett. 351, 375-379, 1994

A;Title: Molecular cloning of a novel candidate G protein-coupled receptor from rat brain

A;Reference number: S48697; MUID:94364507; PMID:8082799

A;Accession: S48697

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-363 <SON>

A;Cross-references: UNIPROT:P51651; UNIPARC:UPI000012BA34; EMBL:U12006; NID:g551333; PID

C;Superfamily: melanocortin receptor

C;Keywords: G protein-coupled receptor

Query Match 18.8%; Score 339.5; DB 2; Length 363;

Best Local Similarity 34.7%; Pred. No. 3.3e-20;

Matches 96; Conservative 51; Mismatches 95; Indels 35; Gaps 12;

Qy 41 VILCCA---IVVENLLVLIIVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLLS---G 94

Db 78 VLLCVSGTVIAGENALVVALIASTPALRTPMFLVGLSATADLLAGCGLLHFVQYVVP 137

Qy 95 SVTLRLTPVQWFAREGSAPITLSASVFSLLAIAIERHVAIAKVLYGSDKS-CRMLLIG 153

Db 138 SETVSLMV-----GFLVASFAASVSLLAITVDRYLSLYNALTYYSRRRTLLGVHLLLA 191

Qy 154 ASWLISVLGGLPIGLWNCGLHLEACSTVPLXAKHYVLCVVTIFSIILLAVVALYVRIY 213

Db 192 ATWTVSLGLGLPIGLWNCGLADRSASVVRPLTSHVAL-LSTSFVFGVGMHLHYVRI- 249

Qy 214 CVVRSSHAD-----MAAPQTLALIK---TVTIVLGVFIVCWLPAFSILLDYACPVH 262

Db 250 QGVVWRHAHQIALQHQCLAPPLAATRAKGVGTAAVLGTGASWLP-PAIY-----CVVG 303

Qy 263 S---CPILYKAHYLFAVSTLNSLNPVIYTWRSRLRR 297

Db 304 SQEDPAIY-TYATLLPATYNSMINPIIYAFRNQBIOR 339

RESULT 13

S36636

melanocortin receptor 3 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: A48254; S36636

R;Roselli-Rehfuess, L.; Mounjojoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatro, J.

Proc. Natl. Acad. Sci. U.S.A. 90, 8856-8860, 1993

A;Title: Identification of a receptor for gamma melanotropin and other proopiomelanocort

A;Reference number: A48254; MUID:94022273; PMID:8415620

A;Accession: A48254

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-323 <ROS>

A;Cross-references: UNIPROT:P32244; UNIPARC:UPI000012ED4C; EMBL:X70667; NID:g396551; PID

A;Note: submitted to the EMBL Data Library, January 1993

A;Note: in Genbank entry RRM33RA, release 113.0, the source is designated as Rattus ratt

C;Genetics:

A;Gene: MC3-R

C;Superfamily: melanocortin receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.7%; Score 338.5; DB 2; Length 323;

Best Local Similarity 32.1%; Pred. No. 3.5e-20; Indels 41; Gaps 11;

Matches 95; Conservative 56; Mismatches 104;

Qy 41 VILCCAIV---VENLLVLIIVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLL-----S 93

Db 44 VFLALGIVSLMENILVILAVVRNGLHSPMYFFLLSLLOADMLVLSLSLETIMIVINS 103

Qy 94 GSVTLRLTPVQWFAREGSAPITLSASVFSLLAIAIERHVAIAKVLYGSDKSCRMILL 151

Db 104 DSLTLEDOFIQHMNDIIFDSMICISLVASICNLLAIAVDVRYVTIFVALRYHSTMTVRKAL- 162

Qy 152 IGASWLSLVLGGLPIGLWNCGLHLEACSTVPLXAKHYVLCVVTIFSIILLAVVALY 209

Db 163 ---SLVAI-----WVCCG---ICGVNFIYVSESKMVICLITMFFAMVLLMGTL 207

Qy 210 VRIYCVVR-----SSHADMAAPQTLALIK---TVTIVLGVFIVCWLPAFSILLDYA 258

Db 208 IHMFLFARLHVQRTAAALPDGVAPOQHSCKGAVTITILGVFFCWAPFLHLVLIIT 267

Qy 259 CPVHSCPILYKAHY---LFAVSTLNSLNPVIYTWRSRLRREVLRLPQCVRPGV 312

Db 268 CPTNPYCICTAHENTYVLVLMCNVIDPLIYAFRSLEL-RNTPKEILCGCGNMV 322

RESULT 14

S40454

G protein-coupled receptor GPCR21 - mouse

C;Species: Mus musculus (house mouse)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:24:31 ; Search time 130 Seconds
(without alignments)
1193.082 Million cell updates/sec

Title: US-10-084-507B-22
Perfect score: 1809
Sequence: 1 MGSLSYSEYLNPNKQEHYNY.....LERGMHMTPTFLEGNTVV 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1809 | 100.0 | 353 | 2 | AAY28289 EDG-4 ami |
| 2 | 1804 | 99.7 | 353 | 2 | AAY49904 Human EDG |
| 3 | 1803 | 99.7 | 353 | 2 | AAY28288 Predicted |
| 4 | 1787 | 98.8 | 353 | 3 | AAB18889 Amino aci |
| 5 | 1787 | 98.8 | 353 | 6 | ABP59285 Human Edg |
| 6 | 1787 | 98.8 | 353 | 6 | ABP59285 Human Edg |
| 7 | 1787 | 98.8 | 353 | 6 | ABP59285 Human Edg |
| 8 | 1787 | 98.8 | 353 | 6 | ABP59285 Human Edg |
| 9 | 1787 | 98.8 | 353 | 7 | ADG11247 Human Edg |
| 10 | 1787 | 98.8 | 353 | 7 | ADG11247 Human Edg |
| 11 | 1787 | 98.8 | 353 | 7 | ADG11247 Human Edg |
| 12 | 1787 | 98.8 | 353 | 8 | ADH57161 Human end |
| 13 | 1787 | 98.8 | 353 | 8 | ADJ62652 Human end |
| 14 | 1787 | 98.8 | 353 | 8 | ADJ62652 Human end |
| 15 | 1787 | 98.8 | 353 | 8 | ADJ62652 Human end |
| 16 | 1787 | 98.8 | 353 | 8 | ADJ62652 Human end |
| 17 | 1787 | 98.8 | 353 | 8 | ADP8359 Human EDG |
| 18 | 1787 | 98.8 | 353 | 8 | ADP8359 Human EDG |
| 19 | 1783 | 98.6 | 353 | 7 | ADP11249 Human EDG |
| 20 | 1755 | 97.0 | 353 | 9 | ADU92079 Human end |
| 21 | 1631.5 | 90.2 | 352 | 3 | AAB03966 Murine ED |
| 22 | 1625.5 | 89.9 | 352 | 2 | AAY58712 Fragment |
| 23 | 1625.5 | 89.9 | 352 | 2 | AAY01663 p(H218), |
| 24 | 1625.5 | 89.9 | 352 | 2 | AAY05492 Human EDG |

| | | | | | | |
|----|--------|------|-----|---|----------|--------------------|
| 25 | 1625.5 | 89.9 | 352 | 2 | AAY87790 | Aaw87790 Rat H218, |
| 26 | 1625.5 | 89.9 | 352 | 4 | AAY00305 | Aau00305 LPA recep |
| 27 | 1625.5 | 89.9 | 352 | 6 | ABU07712 | Abu07712 Rat lysop |
| 28 | 1625.5 | 89.9 | 352 | 6 | ABB98696 | Abb98696 Rat Endot |
| 29 | 1625.5 | 89.9 | 352 | 7 | ABU61816 | Abu61816 Human sph |
| 30 | 1625.5 | 89.9 | 352 | 8 | ADP88361 | Adp88361 Rat endot |
| 31 | 1625.5 | 89.9 | 353 | 7 | ADD48927 | Add48927 Rat Prote |
| 32 | 1622.5 | 89.7 | 352 | 6 | ABB98695 | Abb98695 Murine En |
| 33 | 1622.5 | 89.7 | 352 | 8 | ADO29294 | Ado29294 Mouse GPC |
| 34 | 1509.5 | 83.4 | 377 | 8 | ADP29509 | Adp29509 Human sec |
| 35 | 1432 | 79.2 | 372 | 6 | ABP59289 | Abp59289 Chimeric |
| 36 | 946 | 52.3 | 269 | 4 | ADG15135 | Adg15135 Human 7 t |
| 37 | 946 | 52.3 | 274 | 4 | AAM96680 | Aam96680 Human rep |
| 38 | 946 | 52.3 | 274 | 4 | ABB96585 | Abb96585 Human tes |
| 39 | 946 | 52.3 | 274 | 4 | ADG15162 | Adg15162 Human 7 t |
| 40 | 860.5 | 47.6 | 384 | 6 | ABP59281 | Abp59281 Chimeric |
| 41 | 858.5 | 47.5 | 384 | 6 | ABP59280 | Abp59280 Chimeric |
| 42 | 858 | 47.4 | 391 | 6 | ABP59279 | Abp59279 Chimeric |
| 43 | 854.5 | 47.2 | 362 | 5 | ABG75679 | Abg75679 Human Edg |
| 44 | 854.5 | 47.2 | 362 | 8 | ADO28787 | Ado28787 Arrestin |
| 45 | 854.5 | 47.2 | 362 | 9 | ADX44606 | Adx44606 Chimeric |

ALIGNMENTS

RESULT 1
AAY28289
ID AAY28289 standard; protein; 353 AA.
XX
AC AAY28289;
XX
DT 12-OCT-1999 (first entry)
XX
DE EDG-4 amino acid sequence encoded by clone pC3-hEDG4#36.
XX
KW EDG-4; polypeptide; receptor; inflammation; amino acid; G protein;
KW lysolipid; immune response.
XX
OS Homo sapiens.
XX
PN WO9935259-Al.
XX
PD 15-JUL-1999.
XX
PF 30-DEC-1998; 98WO-CA001195.
XX
PR 30-DEC-1997; 97US-0070185P.
PR 03-APR-1998; 98US-0080610P.
PR 25-NOV-1998; 98US-0109885P.
PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
XX
PI Munroe DG, Kamboj R, Peters D, Kooshesh F, Vyas TB, Gupta AK;
XX
WPI; 1999-430392/36.
XX
PT New isolated lysolipid/EDG receptor useful in the treatment of asthma and
PT rheumatoid arthritis.
PS Claim 7; Fig 16B; 120pp; English.

A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4) . The LL/EDG receptors are involved in an inflammatory response signaling pathway and an apoptotic signaling pathway. They can be used for identifying agonists or antagonists of NF-kB or IL-8 modulated EDG or LL receptors. Agonists can be used for upregulation of an inflammatory process condition or immune response. Antagonists can be used for the downregulation of an inflammatory process condition or immune response. The agonists and antagonists can also be used for controlling apoptosis in a cell comprising the LL/EDG receptor. A diagnostic test for aberrant expression of HEDG-4 can accelerate diagnosis and proper treatment of abnormal conditions of e.g. the heart, kidney, lung and testis. Specific examples

CC of conditions in which aberrant expression of HEDG-4 may play a role
CC include adult respiratory distress, asthma, rheumatoid arthritis, stroke,
CC neurotrauma, Alzheimer's disease, endotoxin shock, atherosclerosis,
CC cardiac ischemia, acute pancreatitis, septic shock, pericarditis, acute
CC cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the
CC liver, and early diabetic glomerulopathy, as well as lung damage
CC following exposure to cigarette smoke, asbestos or silica. HEDG-4
CC specific antibodies, inhibitors, ligands or their analogs can be used as
CC bioactive agents to treat inflammation or disease including viral,
CC bacterial or fungal infections, allergic responses, mechanical injury
CC associated with trauma, hereditary diseases, lymphoma or carcinoma, or
CC other conditions which activate the genes of kidney, lung, heart,
CC lymphoid or tissues of the nervous system
XX

SQ Sequence 353 AA;

Query Match 100.0%; Score 1809; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.1e-177;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKQVQEHYNYTKETLETQETTSRQVASFIVILCCAIIVENLLVLIAR 60
DB 1 MGSLYSEYLNPNKQVQEHYNYTKETLETQETTSRQVASFIVILCCAIIVENLLVLIAR 60
QY 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120
DB 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
QY 181 TVPLPYAKHYVLCVVTIFSIILLAVALYRIYCVVRSSHADMAAPQTALLKTVTVILG 240
DB 181 TVPLPYAKHYVLCVVTIFSIILLAVALYRIYCVVRSSHADMAAPQTALLKTVTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
QY 301 RPLQWRPGVGQRRRGGTGPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
DB 301 RPLQWRPGVGQRRRGGTGPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 2

AA49904
ID AA49904 standard; protein; 353 AA.
XX
AC AA49904;
XX

28-JAN-2000 (first entry)

Human EDG family H218 protein.

KW Human; EDG family; H218; transmembrane receptor protein; diagnosis;
KW therapy; bacterial; fungal; viral; infection; HIV; cancer; diabetes;
KW obesity; anorexia; bulimia; asthma; Parkinson's disease; hypotension;
KW acute heart failure; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; asthma; allergy;
KW benign prostatic hypertrophy; migraine; vomiting; psychotic;
KW neurological disorder; dyskinesia.

OS Homo sapiens.

XX
XX
PN WO9954351-A1.
XX

28-OCT-1999.

14-APR-1999; 99WO-US008099.

23-APR-1998; 98US-0082776P.

PR 03-SEP-1998; 98US-00150650.

XX

(SMIK) SMITHKLINE BEECHAM CORP.

XX Berigsmu DU, Elshourbagy N, Lane P, Li X, Mooney JL, Tsui P;

XX WPI, 1999-633972/54.

DR N-PSDB; AAZ32488.

XX Novel human transmembrane receptor protein for use in treatment and
XX diagnosis of disease.

PS Claim 1; Page 29; 49pp; English.

CC The present sequence is a human EDG family protein designated H218. H218
CC is used for diagnosing disease or its susceptibility in a subject related
CC with expression or activity of H218 by determining the presence or
CC absence of mutation in the polynucleotide encoding H218 in the genome of
CC the subject and/or analysing for the presence of H218 expression in
CC sample derived from the subject. It is also used for treating subjects in
CC need of enhanced activity or inhibition of H218 by administering an
CC agonist or antagonist respectively. H218 can be used to treat abnormal
CC conditions such as bacterial, fungal and viral infections, particularly
CC HIV-1 or 2, cancers, diabetes, obesity, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC stroke, ulcers, asthma, allergies, benign prostatic hypertrophy,
CC migraine, vomiting, psychotic, neurological disorders and dyskinesias can
CC be treated. The H218 polynucleotide can also be used for obtaining
CC hybridisation probes and primers for isolating full-length clones
CC encoding H218. The difference in cDNA or genomic sequence between
CC affected and unaffected individuals is determined to identify mutation
CC causing the disease. It is also valuable for chromosome identification.
CC The polypeptide is used for the identification of membrane bound or
CC soluble receptors through standard receptor binding techniques and also
CC for structure based design of agonist, antagonist or inhibitor of the
CC polypeptides
XX

SQ Sequence 353 AA;

Query Match 99.7%; Score 1804; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 1.7e-176;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKQVQEHYNYTKETLETQETTSRQVASFIVILCCAIIVENLLVLIAR 60
DB 1 MGSLYSEYLNPNKQVQEHYNYTKETLETQETTSRQVASFIVILCCAIIVENLLVLIAR 60
QY 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120
DB 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
QY 181 TVPLPYAKHYVLCVVTIFSIILLAVALYRIYCVVRSSHADMAAPQTALLKTVTVILG 240
DB 181 TVPLPYAKHYVLCVVTIFSIILLAVALYRIYCVVRSSHADMAAPQTALLKTVTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
QY 301 RPLQWRPGVGQRRRGGTGPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
DB 301 RPLQWRPGVGQRRRGGTGPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 3

AA49904

ID AA49904 standard; protein; 353 AA.

XX

AC AA49904;


```
XX 12-OCT-1999 (first entry)
XX Predicted polypeptide product from human EDG-4 cDNA.
XX
XX EDG-4; polypeptide; receptor; inflammation; amino acid; G protein;
XX lysolipid; immune response.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 273
XX /label= unknown
XX /note= "encoded by YTT"
XX
XX WO9935259-A1.
XX
XX 15-JUL-1999.
XX
XX 30-DEC-1998; 98WO-CA001195.
XX
XX 30-DEC-1997; 97US-0070185P.
XX
XX 03-APR-1998; 98US-0080610P.
XX
XX 25-NOV-1998; 98US-0109885P.
XX
XX (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
XX
XX Munroe DG, Kamboj R, Peters D, Kooshesh F, Vyas TB, Gupta AK;
XX
XX WPI; 1999-430392/36.
XX
XX New isolated lysolipid/EDG receptor useful in the treatment of asthma and
XX rheumatoid arthritis.
XX
XX Claim 7; Fig 16A; 120pp; English.
XX
XX A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4). The LL/EDG
XX receptors are involved in an inflammatory response signaling pathway and
XX an apoptotic signaling pathway. They can be used for identifying agonists
XX or antagonists of NF-kB or IL-8 modulated EDG or LL receptors. Agonists
XX can be used for upregulation of an inflammatory process condition or
XX immune response. Antagonists can be used for the downregulation of an
XX inflammatory process condition or immune response. The agonists and
XX antagonists can also be used for controlling apoptosis in a cell
XX comprising the LL/EDG receptor. A diagnostic test for aberrant expression
XX of HEDG-4 can accelerate diagnosis and proper treatment of abnormal
XX conditions of e.g. the heart, kidney, lung and testis. Specific examples
XX of conditions in which aberrant expression of HEDG-4 may play a role
XX include adult respiratory distress, asthma, rheumatoid arthritis, stroke,
XX neurotrauma, Alzheimer's disease, endotoxic shock, atherosclerosis,
XX cardiac ischemia, acute pancreatitis, septic shock, psoriasis, acute
XX cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the
XX liver, and early diabetic glomerulopathy, as well as lung damage
XX following exposure to cigarette smoke, asbestos or silica. HEDG-4
XX specific antibodies, inhibitors, ligands or their analogs can be used as
XX bioactive agents to treat inflammation or disease including viral,
XX bacterial or fungal infections, allergic responses, mechanical injury
XX associated with trauma, hereditary diseases, lymphoma or carcinoma, or
XX other conditions which activate the genes of kidney, lung, heart,
XX lymphoid or tissues of the nervous system
XX
XX Sequence 353 AA;
XX
XX Query Match 99.7%; Score 1803; DB 2; Length 353;
XX Best Local Similarity 99.4%; Pred. No. 2.1e-176;
XX Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MGSLEYLNPKNVQEHYNTKETLETQETTSQVASFIVILCCAIVVENLLVLAVAR 60
XX |||||||
XX 1 MGSLEYLNPKNVQEHYNTKETLETQETTSQVASFIVILCCAIVVENLLVLAVAR 60
XX |||||||
XX 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
XX |||||||
```

```
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLISLVLGGLPILGNWCLHLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLISLVLGGLPILGNWCLHLEACS 180
Qy 181 TVLPLVYAKHYVLGVVTFISIIILLAVVAVLYVRIYCVVRSSHADMAAPQTLLKTTVILG 240
Db 181 TVLPLVYAKHYVLGVVTFISIIILLAVVAVLYVRIYCVVRSSHADMAAPQTLLKTTVILG 240
Qy 241 VFIVCWLPAFSTILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVYIWTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSTILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVYIWTWRSRDLRREVL 300
Qy 301 RPLQWRPQGVQGRRRGTGPHLLPLRSSSSSLERGMHMTPTSFLEGNTVV 353
Db 301 RPLQWRPQGVQGRRRGTGPHLLPLRSSSSSLERGMHMTPTSFLEGNTVV 353

RESULT 4
AAB18889
ID AAB18889 standard; protein; 353 AA.
XX
XX AC AAB18889;
XX
XX DT 08-FEB-2001 (first entry)
XX
XX DE Amino acid sequence of the human Edg5 polypeptide.
XX
XX KW Edg4; Edg5; lysophospholipid receptor; sphingolipid receptor; SIP;
XX KW lysophosphatidic acid; LPA; sphingosine 1-phosphate; gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO200056135-A2.
XX
XX PD 28-SEP-2000.
XX
XX PF 23-MAR-2000; 2000WO-US007649.
XX
XX PR 23-MAR-1999; 99US-00274752.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Goetzl EI, An S;
XX
XX DR WPI; 2000-638230/61.
XX DR N-PSDB; AAA96163.
XX
XX PT Novel human polypeptide receptors for lysophospholipids and
XX PT sphingolipids, native human Edg4, Edg5, mutant of Edg4 comprising
XX PT extended polypeptide tail, used to screen agents that affect LPA and SIP
XX PT activities.
XX
XX Claim 13; Fig 3; 67pp; English.
XX
XX The present sequence represents an Edg polypeptide. The specification
XX describes Edg4 and Edg5 polypeptides. The Edg4 gene is located on
XX chromosome 19p12. The Edg polypeptides are receptors for
XX lysophospholipids and sphingolipids, such as lysophosphatidic acid (LPA)
XX and sphingosine 1-phosphate (SIP). The Edg receptor proteins are used for
XX diagnosing an LPA or SIP mediator condition in an individual. Edg4 and Edg5
XX polypeptides can be used in screening assays designed to determine the
XX effects of a candidate bioactive agent on the expression and activity of
XX Edg4 and Edg5 polypeptides, and the function of LPA and SIP. Nucleotide
XX sequences encoding Edg-4 and Edg-5 are useful as hybridisation probes, in
XX chromosome and gene mapping and in the generation of anti-sense RNA and
XX DNA. Nucleic acids which encode Edg4 or Edg5 or their modified forms can
XX also be used to generate either transgenic animals or knock out animals.
XX Nucleic acid encoding the Edg-4 and Edg-5 polypeptides may also be used
XX in gene therapy
XX
XX Sequence 353 AA;
XX
```


Query Match 98.8%; Score 1787; DB 6; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLYSEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIIVVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFARGSAFILTASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFARGSAFILTASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSKCRMLLLIGASWLSLVLGGLPILGNCGLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSKCRMLLLIGASWLSLVLGGLPILGNCGLHLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTVTVIG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTVTVIG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
DB 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353

RESULT 7
ABU0813
ID ABU0813 standard; protein; 353 AA.
XX ABU0813;
XX 11-AUG-2003 (first entry)
XX Human EDG-5 protein.
XX Human; lymphocyte activation; lymphocyte migration; EDG-5;
KW G-protein coupled receptor; GPCR; lymphocyte; T cell receptor;
KW B cell receptor; CD69; gene therapy; asthma; allergy; autoimmune disease;
KW multiple sclerosis; scleroderma; pernicious anaemia; IDDM;
KW insulin-dependent diabetes mellitus; tissue transplant;
KW graft-versus-host disease; inflammation; infection.
XX Homo sapiens.
XX US2002155512-A1.
XX 24-OCT-2002.
XX 03-OCT-2001; 2001US-00971228.
XX 18-APR-2001; 2001US-0284763P.
XX (RIGB-) RIGEL PHARM INC.
XX Liao XC, Masuda E, Chu P, Pardo J, Li C, Zhao H, Jiang Y;
XX WPI; 2003-340852/32.
XX
XX Identifying lymphocyte modulator activation/migration, by contacting an
PT EDG G-protein coupled receptor polypeptide or cell having the polypeptide
PT with compound and determining chemical/phenotypic effect of compound on
PT cell.
XX
XX Disclosure; Fig 2; 70pp; English.
XX
XX The invention discloses method for identifying a compound that modulates
CC lymphocyte activation/migration. The method comprises contacting an EDG G
CC -protein coupled receptor (GPCR) family polypeptide, or its fragment or a

cell comprising the polypeptide or its fragment with the compound, and
determining the chemical/phenotypic effect of the compound upon the cell.
Also disclosed are methods for modulating lymphocyte activation or
migration in a subject, by administering to the subject a therapeutically
effective amount of an identified compound, an EDG polypeptide or a
nucleic acid encoding an EDG, or its fragment, and for screening for a
modulators of lymphocyte activation, by transfecting into lymphocytes a
cDNA library, stimulating T or B cell receptors of the lymphocytes,
screening for modulation of lymphocyte activation by detecting the level
of CD69 cell surface expression and rescuing cDNAs that modulate
lymphocyte activation. The method is useful for identifying a compound
(such as an antibody, antisense molecule, small organic molecule,
sphingolipid or a sphingolipid analogue) that modulates lymphocyte
activation or migration. The compounds identified are useful for the
treatment (e.g. gene therapy) of diseases such as asthma, allergy,
autoimmune diseases such as multiple sclerosis, scleroderma, pernicious
anaemia, insulin-dependent diabetes mellitus, conditions related to organ
and tissue transplant such as graft-versus-host disease, acute and
chronic inflammation, an infection such as viral, fungal, protozoal or
bacterial infections and diseases in which activation of immune response
and stimulation of lymphocyte migration is desired. The sequence
presented is the human EDG-5 protein

XX Sequence 353 AA;
SQ

Query Match 98.8%; Score 1787; DB 6; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLYSEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIIVVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFARGSAFILTASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFARGSAFILTASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSKCRMLLLIGASWLSLVLGGLPILGNCGLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSKCRMLLLIGASWLSLVLGGLPILGNCGLHLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTVTVIG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTVTVIG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
DB 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353

RESULT 8
ABP82010
ID ABP82010 standard; protein; 353 AA.
XX ABP82010;
XX 04-MAR-2003 (first entry)
XX Human sphingolipid receptor Edg5 protein SEQ ID NO:508.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.

OS WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; ABZ42860.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82016, which are used in the
CC exemplification of the present invention

XX Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 6; Length 353;

Best Local Similarity 98.9%; Pred. No. 9.3e-175;

Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLNPNKQVQEHYNTKETLETQTTTSROVASAFIVILCAIWNLLVLIIVAR 60

DB 1 MGSLSYSLNPNKQVQEHYNTKETLETQTTTSROVASAFIVILCAIWNLLVLIIVAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATITLSASV 120

DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATITLSASV 120

QY 121 FSLIAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSIVLGGIPILGNCLGLEACS 180

DB 121 FSLIAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSIVLGGIPILGNCLGLEACS 180

QY 181 TVLFLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSHADMAAPQTLALLKTTVILG 240

|||||

DB 181 TVLFLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSHADMAAPQTLALLKTTVILG 240

QY 241 VFIVCWLPAPFSIILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

DB 241 VFIVCWLPAPFSIILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPVGVGQRRRGTFPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

DB 301 RPLQWRPVGVGQRRRGTFPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

RESULT 9

ADC40485

ID ADC40485 standard; protein; 353 AA.

XX ADC40485;

XX 18-DEC-2003 (first entry)

XX Protein of human EDG-5.

XX gene expression analysis; collective quantitative analysis;

KW G protein coupled receptor; tyrosine oxidase receptor family;

KW ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis;

KW myocardial infarction; infarct; ischaemic disease; GPCR; human; EDG-5.

XX Homo sapiens.

XX WO2003052096-A1.

XX 26-JUN-2003.

XX 13-DEC-2002; 2002WO-JP013097.

XX 14-DEC-2001; 2001JP-00382053.

PR 21-FEB-2002; 2002JP-00045104.

PR 15-MAY-2002; 2002JP-00140111.

PR 18-NOV-2002; 2002JP-00333769.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hinuma S, Kobayashi M, Arai T, Fukusumi S, Fujii R, Komatsu H;

PI Matsumura F, Kawamata Y, Ogi K;

XX WPI; 2003-533023/50.

DR N-PSDB; ADC40486.

XX Method for gene expression analysis for treatment of cancers.

PS Disclosure; SEQ ID NO 46; 261pp; Japanese.

XX The invention relates to a novel method for gene expression analysis by
CC collective quantitative analysis of the expression of a number of genes
CC to identify those that are promoted or inhibited in a given cell or
CC tissue. The genes are preferably gene families such as the G protein
CC coupled receptor family, tyrosine oxidase receptor family, or ion channel
CC gene family. The methods may be used in treatment of cancers, including
CC prostate, ovarian, stomach, bladder, breast, and cancer of the
CC intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used
CC in the treatment and prevention of atherosclerosis, myocardial
CC infarction, infarct or ischaemic disease of the brain. This sequence
CC represents a protein of human EDG-5 of the invention.

XX Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 7; Length 353;

Best Local Similarity 98.9%; Pred. No. 9.3e-175;

Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLNPNKQVQEHYNTKETLETQTTTSROVASAFIVILCAIWNLLVLIIVAR 60

DB 1 MGSLSYSLNPNKQVQEHYNTKETLETQTTTSROVASAFIVILCAIWNLLVLIIVAR 60

QY 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
 Db NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
 QY 121 FSLLAIAERHVAIAKVKYSGDKSCRMILLIGASWLSLVGGLPILGWNCLGHEACS 180
 Db 121 FSLLAIAERHVAIAKVKYSGDKSCRMILLIGASWLSLVGGLPILGWNCLGHEACS 180
 QY 181 TVPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTTVIVLG 240
 Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTTVIVLG 240
 QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
 Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
 QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGHMHMPTSPTFLEGNTVV 353
 Db 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGHMHMPTSPTFLEGNTVV 353

RESULT 10
 ADD11247
 ID ADD11247 standard; protein; 353 AA.
 XX
 AC ADD11247;
 DT 01-JAN-2004 (first entry)
 XX
 DE Human EDG5 protein SEQ ID NO:3.
 XX
 KW Type II diabetes mellitus; venous thrombosis; pulmonary embolism; EDG5;
 KW EDG5 V286A; antidiabetic; thrombolytic; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003085130-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 07-APR-2003; 2003WO-BF003569.
 XX
 PR 09-APR-2002; 2002EP-00007879.
 XX
 PA (AVET) AVENTIS PHARMA DEUT GMBH.
 XX
 PI Kozian D, Kostenis E, Siegler K, Jacobs M, Deleuze J, Ricard S;
 PI Mace S;
 DR WPI; 2003-804314/75.
 DR N-PSDB; ADD11248.
 XX
 PT Identifying an increase in risk for Type II diabetes mellitus and/or
 PT venous thrombosis/pulmonary embolism comprises determining in a probe the
 PT presence of amino acid exchange at position 286 from Val to Ala in the
 PT EDG5 protein.
 XX

PS Example 2; SEQ ID NO 3; 21pp; English.
 XX
 CC The present invention describes a method for identifying an increase in
 CC risk for Type II diabetes mellitus and/or venous thrombosis/pulmonary
 CC embolism, comprising determining the presence of amino acid exchange at
 CC position 286 from Val to Ala in the EDG5 protein. Also described: (1) a
 CC method for screening pharmaceuticals useful for treating and/or
 CC preventing type II diabetes and/or venous thrombosis/pulmonary embolism,
 CC where a cell or cell extract is used that contains EDG5 with the amino
 CC acid exchange, or the variation in the nucleotide sequence of EDG5
 CC protein or the EDG5-286-AA; (2) a method for adapting the dosage of the
 CC pharmaceutical described above by testing the human cell for the presence
 CC of EDG5 with the amino acid exchange, or the variation in the nucleotide
 CC sequence of EDG5 protein or the EDG5-286-AA; (3) a method of selecting
 CC patients who will respond type II diabetes and/or venous
 CC thrombosis/pulmonary embolism by testing the probe of the respective

CC patient for the presence of EDG5 with the amino acid exchange, or the
 CC variation in the nucleotide sequence of EDG5 protein or the EDG5-286-AA;
 CC and (4) a test kit for testing the presence of the amino acid exchange,
 CC or the variation in the nucleotide sequence of EDG5 protein or the EDG5-
 CC 286-AA. EDG5 has antidiabetic and thrombolytic activities, and can be
 CC used in gene therapy. The methods are useful for identifying an increase
 CC in risk for type II diabetes mellitus and/or thrombosis/pulmonary
 CC embolism, and for screening pharmaceuticals useful for treating type II
 CC diabetes mellitus and/or venous thrombosis/pulmonary embolism. The
 CC methods are also useful for adapting the dosage of a pharmaceutical
 CC useful for treating the above diseases. The methods are useful for
 CC selecting patients who will respond to the pharmaceutical. The present
 CC sequence represents the human EDG5 protein, which is used in an example
 CC from the present invention.

SQ Sequence 353 AA;
 Query Match 98.8%; Score 1787; DB 7; Length 353;
 Best Local Similarity 98.9%; Pred. NO. 9.3e-175;
 Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGSLSYSEYLNPNKQOEHYNTKETLETTSTROVASAFIVILCCAIIVVENLLVIAVAR 60
 Db 1 MGSLSYSEYLNPNKQOEHYNTKETLETTSTROVASAFIVILCCAIIVVENLLVIAVAR 60
 QY 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
 Db 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
 QY 121 FSLLAIAERHVAIAKVKYSGDKSCRMILLIGASWLSLVGGLPILGWNCLGHEACS 180
 Db 121 FSLLAIAERHVAIAKVKYSGDKSCRMILLIGASWLSLVGGLPILGWNCLGHEACS 180
 QY 181 TVPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTTVIVLG 240
 Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTTVIVLG 240
 QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
 Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
 QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGHMHMPTSPTFLEGNTVV 353
 Db 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGHMHMPTSPTFLEGNTVV 353

RESULT 11
 ADD90760
 ID ADD90760 standard; protein; 353 AA.
 XX
 AC ADD90760;
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Edg5 receptor.
 XX
 KW receptor; human; Edg5 receptor; gastrointestinal disorder;
 KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
 KW asthma; immune disorder; cognitive disorder; memory disorder; obesity;
 KW pain; psychotic behaviour; affective disorder; migraine; cancer; AIDS;
 KW wound healing; ischaemia-reperfusion injury-related disease.
 XX
 OS Homo sapiens.
 XX
 PN US2003130493-A1.
 PD 10-JUL-2003.
 XX
 PF 26-AUG-2002; 2002US-00228762.
 XX
 PR 22-FEB-1999; 99US-00253998.
 PR 16-JUL-1999; 99US-00356315.
 XX

PA (BONI/) BONINI J A.
PA (HUAN/) HUANG L Y.
PA (BORO/) BOROWSKY B E.
PA (SALO/) SALON J A.
PA (WILS/) WILSON A.
PA (NAGO/) NAGORNY R.
XX
XX
PI Bonini JA, Huang LY, Borowsky BE, Salon JA, Wilson A, Nagorny R;
XX WPI; 2003-829581/77.
XX
XX New mammalian Edg7 receptor proteins and nucleic acids encoding mammalian
PT Edg7 receptors, useful for diagnosing and treating an abnormality
PT associated with the activity of the mammalian Edg7 receptor, e.g. asthma,
PT migraine or cancer.
XX
XX Disclosure; SEQ ID NO 19; 64pp; English.
PS
XX The invention relates to an isolated nucleic acid encoding a mammalian
CC Edg7 receptor. The mammalian Edg7 receptor proteins and nucleic acid
CC encoding the proteins are useful for diagnosing and treating an
CC abnormality associated with the activity of the mammalian Edg7 receptors,
CC e.g. gastrointestinal disorder, a cardiovascular disorder, hypertension,
CC diabetes, respiratory disorder, asthma, immune disorder, cognitive
CC disorder, memory disorder, obesity, pain, psychotic behaviour, affective
CC disorder, migraine, cancer, AIDS, wound healing, or ischaemia-reperfusion
CC injury-related diseases. The nucleic acids and proteins are also useful
CC for developing and designing drugs with higher specificity and fewer side
CC effects. The nucleic acid probes are useful for detecting nucleic acid
CC encoding mammalian Edg7 receptors and antisense oligonucleotides
CC complementary to the nucleic acid sequences. The methods are also useful
CC for identifying agonists and antagonists of Edg7 receptors. The present
CC sequence represents the amino acid sequence of the human Edg5 receptor.
XX
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 7; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
DB 1 MGSLSYSLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLILGNWCLGHLRACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLILGNWCLGHLRACS 180

QY 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALLKTTVIVLG 240
DB 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALLKTTVIVLG 240

QY 241 VFVLCWLPAFSILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRLRREVL 300
DB 241 VFVLCWLPAFSILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRLRREVL 300

QY 301 RPLQWRPGVGQGRRRGTGPHLLPLRSSSLERGMHMTPTFLEGNTVV 353
DB 301 RPLQWRPGVGQGRRRGTGPHLLPLRSSSLERGMHMTPTFLEGNTVV 353

RESULT 12
ADH57161
ID ADH57161 standard; protein; 353 AA.
XX
XX ADH57161;
XX
DT 25-MAR-2004 (first entry)
XX

DE Human endothelial differentiation factor 5 (EDG5) protein SeqID 3.
XX
KW G protein coupled receptor; EDG5; type II diabetes mellitus;
KW venous thrombosis; pulmonary embolism; endothelial differentiation gene;
KW EDG.
XX
OS Homo sapiens.
XX
XX US2003219808-A1.
FN
XX 27-NOV-2003.
PD
XX 21-MAR-2003; 2003US-00393870.
PF
XX 09-AUG-2002; 2002US-0402305P.
PR
XX (KOZI/) KOZIAN D.
PA (KOST/) KOSTENIS E.
PA (SIEG/) SIEGLER K.
PA (JACO/) JACOBS M.
PA (DELE/) DELEUZE J.
PA (RICA/) RICARD S.
PA (MACE/) MACE S.
XX
PI Kozian D, Kostenis E, Sieglér K, Jacobs M, Deleuze J, Ricard S;
PI Mace S;
XX
XX WPI; 2004-060183/06.
DR N-PSDB; ADH57162.
XX
XX Identifying an increase in risk for type II diabetes mellitus, venous
PT thrombosis, pulmonary embolism or its combination in subject by
PT determining whether amino acid residue at position 286 of EDG5 protein is
PT alanine.
XX
XX Example 2.4; SEQ ID NO 3; 10pp; English.
PS
XX This invention relates to a novel method for identifying an increase in
CC risk for type II diabetes mellitus, venous thrombosis, pulmonary embolism
CC or a combination thereof. Specifically, it refers to a the endothelial
CC differentiation gene 5 (EDG5) located on chromosome 19p13.2, which
CC encodes a G protein coupled receptor protein. The present invention
CC describes an immunochemically reactive labelled antibody based kit that
CC can be used to identify the Val286Ala variation in the EDG5 protein
CC encoded by a single nucleotide polymorphism. Furthermore, this allele
CC encoding the V286A variant represents a genetic marker that can be useful
CC for preventative treatments of the aforementioned diseases, as well as
CC for adapting drug dosage for patients, for drug screening purposes or for
CC patient selection in phase or clinical studies. This polypeptide sequence
CC is the human EDG5 protein of the invention.
XX
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 8; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
DB 1 MGSLSYSLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLILGNWCLGHLRACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLILGNWCLGHLRACS 180

QY 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALLKTTVIVLG 240
DB 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALLKTTVIVLG 240

| | | | | | | |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|---------------------|-----------|-------------|--|
| PT | compounds that modulates diagnosing and treating disease condition | | | | | |
| PT | associated with GPCR dysfunction e.g. autoimmune diseases, angina | | | | | |
| PT | pectoris, Parkinson's disease. | | | | | |
| XX | | | | | | |
| PS | Claim 151; SEQ ID NO 394; 542bp; English. | | | | | |
| XX | | | | | | |
| CC | The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several GPCR genes, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridize to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus, and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. | | | | | |
| XX | | | | | | |
| SQ | Sequence 353 AA; | | | | | |
| | Query Match | 98.8%; | Score 1787; | DB 8; | Length 353; | |
| | Best Local Similarity | 98.9%; | Pred. No. 9.3e-175; | | | |
| | Matches 349; | Conservative 1; | Mismatches 3; | Indels 0; | Gaps 0; | |
| QY | 1 | MGLSYEYNPNKVOEHNYTKETLETQETTSROVASAFIVLCCALVVENLLVLAVAR | 60 | | | |
| Db | 1 | MGLSYEYNPNKVOEHNYTKETLETQETTSROVASAFIVLCCALVVENLLVLAVAR | 60 | | | |
| QY | 61 | NSKFHSAMYLFLGNLAASDLLAGVAFAVNTLLSGSVTLRLTPVQWFAREGSAPITLSASV | 120 | | | |
| Db | 61 | NSKFHSAMYLFLGNLAASDLLAGVAFAVNTLLSGSVTLRLTPVQWFAREGSAPITLSASV | 120 | | | |
| QY | 121 | FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLIISLVGGLPILGWNCIGHLEACS | 180 | | | |
| Db | 121 | FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLIISLVGGLPILGWNCIGHLEACS | 180 | | | |
| QY | 181 | TVLPLYAKHYLCVVVTIFSIILLAAVALYVRIYCVRESSHADWAAPQTALLKTVTIVLG | 240 | | | |
| Db | 181 | TVLPLYAKHYLCVVVTIFSIILLAAVALYVRIYCVRESSHADWAAPQTALLKTVTIVLG | 240 | | | |
| QY | 241 | VFTVCWLPAFSLILDLDYACPVHSCPILYKAHYLFVAVSTLNLSLNPIVITYWRSRDLRREV | 300 | | | |
| Db | 241 | VFTVCWLPAFSLILDLDYACPVHSCPILYKAHYFFAVSTLNLSLNPIVITYWRSRDLRREV | 300 | | | |
| QY | 301 | RPLQCWRPGVGQRRRGTTGHHLLPLRSSSSSLERGMHMPTGPTFLEGNTTV | 353 | | | |
| Db | 301 | RPLQCWRPGVGQRRRGTTGHHLLPLRSSSSSLERGMHMPTGPTFLEGNTTV | 353 | | | |
| RESULT 15 | | | | | | |
| AD057997 | | | | | | |
| ID | AD057997 standard; protein; 353 AA. | | | | | |
| XX | | | | | | |

CC Chronic obstructive pulmonary disease. The nucleotide sequences encoding
CC EDG5 are useful as hybridization probes, in constructing oligomers for
CC PCR, for chromosome and gene mapping, in the recombinant production of
CC EDG5, in generating antisense DNA or RNA and in molecular biology
CC techniques that have not yet been developed. EDG5 polypeptides are useful
CC for immunising a mammal to produce polyclonal antibodies and for
CC diagnostic purposes. This sequence represents the human EDG5 receptor
CC protein of the invention.
XX
XX
SQ Sequence 353 AA;

| | | | | | |
|-----------------------|-----|--------------------------------------------------------------|---------------------|-----------|-------------|
| Query Match | | 98.8%; | Score 1787; | DB 8; | Length 353; |
| Best Local Similarity | | 98.9%; | Pred. No. 9.3e-175; | | |
| Matches 349; | | Conservative 1; | Mismatches 3; | Indels 0; | Gaps 0; |
| QY | 1 | MGSLYSEYLNPNKQVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVVENLLVLIAR | 60 | | |
| DB | 1 | MGSLYSEYLNPNKQVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVVENLLVLIAR | 60 | | |
| QY | 61 | NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAPITLSASV | 120 | | |
| DB | 61 | NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAPITLSASV | 120 | | |
| QY | 121 | FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLIISLVLGGLPILGWNCLGHEACS | 180 | | |
| DB | 121 | FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLIISLVLGGLPILGWNCLGHEACS | 180 | | |
| QY | 181 | TVLPLYAKHYVLCVVTIFSIILLAVVALVRIYCVVRSSHADMAAPQTALLKTTIVLG | 240 | | |
| DB | 181 | TVLPLYAKHYVLCVVTIFSIILLAVVALVRIYCVVRSSHADMAAPQTALLKTTIVLG | 240 | | |
| QY | 241 | VFTVCWLPAPFILLDDYACPVHSCPTLYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL | 300 | | |
| DB | 241 | VFTVCWLPAPFILLDDYACPVHSCPTLYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL | 300 | | |
| QY | 301 | RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMHPTSPTFLEGNTVV | 353 | | |
| DB | 301 | RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMHPTSPTFLEGNTVV | 353 | | |

Search completed: December 4, 2005, 06:46:54
Job time : 131 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:23:26 ; Search time 6 Seconds
(without alignments)
281.714 Million cell updates/sec

Title: US-10-084-507B-17

Perfect score: 1806

Sequence: 1 MGSLSYSEVLPNKKQEHYNY.....LERGWHMPTSPFLEGNTVV 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1 | 504 | 27.9 | 364 | 7 US-11-067-884-2 | Sequence 2, Appli |
| 2 | 484 | 26.8 | 351 | 7 US-11-067-884-4 | Sequence 4, Appli |
| 3 | 480.5 | 26.6 | 353 | 7 US-11-067-884-6 | Sequence 6, Appli |
| 4 | 286 | 15.8 | 360 | 6 US-10-851-667A-26 | Sequence 26, Appli |
| 5 | 224.5 | 12.4 | 430 | 6 US-10-992-577-8 | Sequence 8, Appli |
| 6 | 213.5 | 11.8 | 432 | 6 US-10-992-577-2 | Sequence 2, Appli |
| 7 | 204.5 | 11.3 | 420 | 6 US-10-992-577-6 | Sequence 6, Appli |
| 8 | 204.5 | 11.3 | 522 | 6 US-10-510-018-2 | Sequence 2, Appli |
| 9 | 199.5 | 11.0 | 417 | 6 US-10-992-577-44 | Sequence 44, Appli |
| 10 | 196 | 10.9 | 440 | 6 US-10-502-893-2 | Sequence 2, Appli |
| 11 | 184 | 10.2 | 342 | 6 US-10-980-388-118 | Sequence 118, App |
| 12 | 184 | 10.2 | 419 | 7 US-11-067-884-8 | Sequence 8, Appli |
| 13 | 167.5 | 9.3 | 508 | 6 US-10-980-388-112 | Sequence 112, App |
| 14 | 141 | 7.8 | 415 | 6 US-10-627-633-2 | Sequence 2, Appli |
| 15 | 140 | 7.8 | 485 | 6 US-10-821-234-934 | Sequence 934, App |
| 16 | 139 | 7.7 | 313 | 7 US-11-095-093-2 | Sequence 2, Appli |
| 17 | 134 | 7.4 | 409 | 6 US-10-627-633-4 | Sequence 4, Appli |
| 18 | 124.5 | 6.9 | 340 | 6 US-10-980-388-117 | Sequence 117, App |
| 19 | 124.5 | 6.9 | 352 | 6 US-10-627-633-6 | Sequence 6, Appli |
| 20 | 122 | 6.8 | 287 | 6 US-10-980-388-66 | Sequence 66, Appli |
| 21 | 122 | 6.8 | 352 | 7 US-11-068-686-20 | Sequence 20, Appli |
| 22 | 121 | 6.7 | 352 | 7 US-11-068-686-2 | Sequence 2, Appli |
| 23 | 115 | 6.4 | 355 | 7 US-11-068-686-4 | Sequence 4, Appli |
| 24 | 109.5 | 6.1 | 350 | 6 US-10-502-145-1 | Sequence 1, Appli |
| 25 | 107 | 5.9 | 347 | 6 US-10-131-826A-18 | Sequence 18, Appli |

Sequence 119, App
Sequence 100, App
Sequence 68, Appl
Sequence 115, App
Sequence 199, App
Sequence 8, Appli
Sequence 63, Appli
Sequence 96, Appl
Sequence 116, App
Sequence 444, App
Sequence 2566, Ap
Sequence 402, App
Sequence 201, App
Sequence 3306, Ap
Sequence 950, App
Sequence 7826, Ap
Sequence 13, Appl
Sequence 230, App
Sequence 174, App
Sequence 2026, Ap

ALIGNMENTS

RESULT 1

US-11-067-884-2

; Sequence 2, Application US/11067884

; Publication No. US20050261252A1

; GENERAL INFORMATION:

; APPLICANT: Miller, Duane D.

; APPLICANT: Tigvi, Gabor

; APPLICANT: Dalton, James T.

; APPLICANT: Sardar, Vineet M.

; APPLICANT: Elrod, Don B.

; APPLICANT: Xu, Huiping

; APPLICANT: Baker, Daniel L.

; APPLICANT: Wang, Dean

; APPLICANT: Lilio, Karoly

; APPLICANT: Fischer, David J.

; APPLICANT: Virag, Tamas

; APPLICANT: Nusser, Nora

; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF

; FILE REFERENCE: 20609/305

; CURRENT APPLICATION NUMBER: US/11/067,884

; PRIOR FILING DATE: 2005-02-28

; PRIOR FILING DATE: 2000-03-17

; PRIOR FILING DATE: 2001-03-19

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 2

; LENGTH: 364

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-067-884-2

Query Match 27.9%; Score 504; DB 7; Length 364;

Best Local Similarity 34.3%; Pred. No. 6.4e-36;

Matches 116; Conservative 71; Mismatches 121; Indels 30; Gaps 9;

QY 18 YNYKTELETQTTTSRQVASFIVILCAIVVENLLVLIANRNSKFSAMVLFGLNLA 77

Db 34 YNRSGKHLATENWTVSKLVMLGITVCIFIMLANLVNVAIVNRRFFPIYLLMANLA 93

QY 78 SLLAGVAFVANTLLSGSVTLRLTPQWFAREGSFATLSASFVSLLAIAIERHVAIAKV 137

Db 94 ADFFAGLAYFYIMFNTGNTGNTRLTVSTWLLRQGLDITSLTASVANLLAIAIERHTVFRM 153

QY 138 KLYGSDKSCRMILLIGASWLSISLVGLGPIFGWNCGLHLEACSTVLPYAKHYVLCWVTI 197


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; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-8

```

| | | | | | | | |
|-----------------------|--------|--------------|----------|------------|------|--------|------|
| Query Match | 12.4%; | Score | 224.5; | DB | 6; | Length | 430; |
| Best Local Similarity | 24.3%; | Pred. No. | 2.6e-12; | | | | |
| Matches | 99; | Conservative | 59; | Mismatches | 128; | Indels | 121; |
| Gaps | 17; | | | | | | |

| | | | | | | | |
|----|-----|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----|
| Qy | 35 | VASAFVILCAIWENLLVLI | AVARNSKPFSAMYFL | GLNLAA | SDLLAGVAF | AVANTLLSG | 94 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Db | 48 | VAYALFLLC--WVGN | TYCFVLKRNHMTVTN | MFILNAV | SDLLVGIFC | MTTLDVN | 104 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Qy | 95 | SVTLRLTPQVFA | REGSAP----- | ITLSAS | VFSLLAIA | IER----- | 136 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Db | 105 | LIT----- | GWPF | NATCKMSGLVQ | GSVSASVETL | VAIAVERFCI | 152 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Qy | 137 | VKLYGSDKSCRM | LLLTGASNLISLV | ---GGL | PLIGWNC | LGH---LEAC | 191 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Db | 153 | LTLR----- | KALVT | AVIWA | LLALMLCPS | AVILTVT | 202 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Qy | 192 | LC----- | VVTIFS | IIALLAIV | ALVRIYCV | VR----- | 225 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Db | 203 | CWEA | WPCKGMRRVY | TVTLF | SHIYLA | PLALIVMY | 261 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Qy | 226 | PQTALLKTV | TVILGVFI-- | VCWLP | APSFILL-- | DY---ACP | 280 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Db | 262 | SRRARV | VHMLVMVALF | TLSW | PLWALL | LLIDYQL | 321 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Qy | 281 | SLANP | VITYWRS | DLRR-- | EVLRL | PCQWRP | 308 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Db | 322 | SSANPI | YGYFNENFR | RGFOAA | FRALCP | PPSG | 381 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Qy | 309 | GVGVQ | RRRGCTPG | HLLPL | URSS | SSSL | 346 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |
| Db | 382 | GLP | SESGP | SCAPR | GPLRN | RGVAH | 428 |
| | | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | : : : : : : : : : : : | |

```

RESULT 6
US-10-992-577-2
; Sequence 2, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-992-577-2

```


QY 251 STILL-DYA-CPVHSCPIYKAHYFA--VSTLSILLNPVIYTWRSRLR 297
Db 394 TLWMLSDYADLSFNLQIINIYIPFAHWLAFGSSVNPIIYGFNFR 444

RESULT 9

US-10-992-577-44
; Sequence 44, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Bayer HealthCare AG
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with a New
; TITLE OF INVENTION: Human SHT6 Receptor
; FILE REFERENCE: LeA 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-502-893-2

Query Match 11.0%; Score 199.5; DB 6; Length 417;
Best Local Similarity 22.7%; Pred. No. 3.2e-10;
Matches 88; Conservative 74; Mismatches 123; Indels 103; Gaps 17;
QY 20 YTKETLETQETSROVASAFIVLCCAIIVVENLLVIAVARNSKFSAMYLFLGNLAASD 79
Db 34 YNYYLHQHVTAVPFISSVFLFFLC--WGNVTVCVIRNRYMTVTNFIENLAISD 91
QY 80 LLGAVFANTLLS-----GSVTLRLTPVQWFAREGSFITLSASVFSLLAIAIERH 131
Db 92 LLVGIFCMPITLLDNIAGWPFGSSMCKISGLV---QG---ISVAASVETLVAIAVDRF 144
QY 132 VAIA---KVKLYGSDSKRCMLLLIGASWLSISLVGLPIL----- 168
Db 145 RCVVYFPFKP-----LTVKTAFVNIIVINGLAITIMTPSAIMLHVQEEKYRVR 193
QY 169 --GWNCLGHLEAGSTVPLKHYHVLGVTVFISILLAIYALVYVRYCVVRS----- 219
Db 194 LSHNKTSTVYWCREDWPNQEMRIYTV-LFATYIPLSLIVIMYRIGASLFKTSAH 252
QY 220 -----HADMAAPQTLALKTVTIVLGVFVLCWLPAPFSLILL-DYA-CPVHSCPI 267
Db 253 STGKQRLQEWHSKQKQKMLTVAL--LFILSWLPLWTLMLSDYADLSPNKLRVI 309
QY 268 YKAHYFA--VSTLSILLNPVIYTWRSRLR-----REVLPLOCWRPGVQVGR 315
Db 310 NIYVYFAHWLAFNCFSVNPPIYGFNFNFRSGFDQFQCKKVKQEAY-----GLRAK 365
QY 316 RRGGTPGHLLPLRSSSSSLRGMHMTS 343
Db 366 RN-----LDINTSGLL---VHEPAS 382

RESULT 10

US-10-502-893-2
; Sequence 2, Application US/10502893

; Publication No. US20050255529A1
; GENERAL INFORMATION:
; APPLICANT: Bayer HealthCare AG
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with a New
; TITLE OF INVENTION: Human SHT6 Receptor
; FILE REFERENCE: LeA 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-502-893-2

Query Match 10.9%; Score 196; DB 6; Length 440;
Best Local Similarity 25.5%; Pred. No. 6.7e-10;
Matches 96; Conservative 51; Mismatches 135; Indels 94; Gaps 17;
QY 35 VASAFIVLCCAIIVVENLLVLI-----AVARNKFSAMYLFLGNLAASDLLAGVAF--- 86
Db 29 VAAALCVVIALTAANAANSLIALICTQPALRNTSNF-----PLVSLFTSMLMVLVWMP 82
QY 87 -VANTLLSGSVTLRLTPVQWFAREGSFITLSASVFSLLAIAIERHVAIAKLYGSDKS 145
Db 83 AMLNLYGRWVLARGCLLWTFD---VMCCSASINCLISLDYLLLSPLRYKLRT 139
QY 146 -CRMILLIGASWLSISLVGLP-ILGWNCLGHLE-----ACSTVLPYKHYHVLGVTVI- 197
Db 140 PLRALALVIGASWLSLAALASFLPLLGHGHELGHARPPVPGQCRLLASL---PFVLVASGLT 196
QY 198 FSIIILLAIYALVYVRYCVVRSADMA-----AQTLAL----- 231
Db 197 FFLPSGAICFTYCRILLAARKQAVQVASTTGMASQASSETLQVPRTPRGVSASRRRLA 256
QY 232 -----LK---TVTVLGVFVLCWLPAPFISILLDYACPVHSCPIYKHYHFAVST--- 278
Db 257 TKHSRKALKASUTLGLGMFFVTLPPFVANIIVQAVDCIS-PGL-----FDVLTWLG 309
QY 279 -LNSLLNPVIYTWRSRLRREVLRLQCVW-----PGVGVQRRRGGTGPHHLLPL 328
Db 310 YCNSTMNPIIYPLFMRDFKRALGRFLPCPCPRERQASLASPSLRTSHSGPRPG----- 363
QY 329 RSSSSSLRGMHMTSP 344
Db 364 ---LSLQVLPPLPP 376

RESULT 11

US-10-980-388-118
; Sequence 118, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.01
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02

```
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-980-388-118

Query Match      10.2%; Score 184; DB 6; Length 342;
Best Local Similarity 22.4%; Pred. No. 5,2e-09;
Matches 64; Conservative 53; Mismatches 103; Indels 66; Gaps 11;

Qy 48 VVENLLVLIIVARNKSFHMYFLGNLAASDLGAGVAVANTLLSGSVTLRLTFVQWFA 107
Db 46 VFGNLLVMTSVLHFQKLSPTNFIASLACADFLVGVTVMLFSM-----VRTVESCWYF 99

Qy 108 REGSAFITS-----ASVFSLLAIAERHVAIAKVLGSKRCML-LILGASWL 157
Db 100 --GAKFCTLLSCDDVAFCYSSVHLHCFICIDRIYIVTDPVLYATKFTVSVSGICISVSI 157

Qy 158 ISLVGLGLP-----ILGNCLGHLEACSTVPLVYAKHYVLCVVTIFSIIILA 204
Db 158 LPLTYSAGVFTGVNDDGLEHLSALNCVG---GCQIIV---SQGWLIDFLFFIFTLV 211

Qy 205 IVALYVRYICVVR-----SSHADMAAPOTLALLKTVITVLGVFVFCWL 247
Db 212 MILYSKIFLIAKQQAIIETTSSKVESSESYKIRVAKRERKAAKTLGVTVLAFVISWL 271

Qy 248 PAFSILLD-----YACPVHSCPI-LYKAHYXFAVSTLNSLNPVIY 288
Db 272 PYTVDLIDAFMGFLTPAYIIEICWSAY-----NSAMNPLIY 310

RESULT 12
US-11-067-884-8
; Sequence 8, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Tigyi, Duane D.
; APPLICANT: Miller, Gabor
; APPLICANT: Daiton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lilom, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Nusser, Tamas
; APPLICANT: Nura
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
```

```
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-067-884-8

Query Match      10.2%; Score 184; DB 7; Length 419;
Best Local Similarity 25.5%; Pred. No. 6.5e-09;
Matches 92; Conservative 49; Mismatches 132; Indels 88; Gaps 17;

Qy 37 SAFIVILCCAIVVENLLVLIIVARNKSFHMYFLGNLAASDLGAGV---AFVANTLLS 93
Db 85 SAIMIFILFVSFLGNLVCLMVYQKAAMRSAINILLASLAFADMLLAVLNMPFALVTIL- 143

Qy 94 GSVTLRLTPVQWFAREGSAFITLSA--SVFSLAIAIERHVAIA---KVKLYGSDKSCR 147
Db 144 ---TTRWIFGKFCRVSMFVFLVIEGVAILLIISIDRELIIVORQDKLNPY-----R 194

Qy 148 MLLIGASWLIS-----LVLGG---LPLGNWCL-GHLEACSTVPLVYAKHYVLCVVT 196
Db 195 AKVLIIVSWATSFVCAVPLAVGNPDQLQPSRAPQCVFGY-----TTNFGYQAVVILISLI 249

Qy 197 IFSILLIAIV-----ALYVRIY---CVVRSSHADMAAPQ-----T 228
Db 250 SFFIPFVLIVSYFMGILNTHRNALRIHSPYEGICLSQASKGLMSLQRPQMSIDMGFK 309

Qy 229 LALLKTVITVLGVFVFCWLPAFSTILLDYACPVHSCPILYKAHYXFAVST-----LNS 281
Db 310 TRAFFTLLIFANFIVCWAP-FTTYSLVATFSKH---FYQHNFFEISTWLLWLCVLKS 364

Qy 282 LLNPVYTWRSR---DLRREVLRLPQCWRPGVGVQRRRGRTPGHLLPLRSSSSLSRGM 338
Db 365 ALNPLIYYWRIKRPKPHDACLDMMPKSKFLPQL-----PGHTRRIRPSAVYVCGE 414

Qy 339 H 339
Db 415 H 415

RESULT 13
US-10-980-388-112
; Sequence 112, Application US/10980388
; Publication No. US2005025490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
```



```
/ PRIOR APPLICATION NUMBER: 60/184,397
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,247
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/188,880
/ PRIOR FILING DATE: 2000-03-13
/ PRIOR APPLICATION NUMBER: 60/217,369
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/217,370
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/218,492
/ PRIOR FILING DATE: 2000-07-20
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 184
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 112
/ LENGTH: 508
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-980-388-112

Query Match          9.3%; Score 167.5; DB 6; Length 508;
Best Local Similarity 24.7%; Pred. No. 2e-07;
Matches 49; Conservative 48; Mismatches 84; Indels 17; Gaps 6;

QY 35 VASAFITLCCATWENLVLIAVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLLS 94
DB 33 IRSTVLVIFLASFGVGNIVLALVLRKPOLLOVTRNFNLVTDLLQ-LSLVAPWVAT 91

QY 95 SVTLRTPVQWFAREG--SAFITLS-----ASVFSLLAIAIERHVAIAKVLGYGDKSCR 147
DB 92 SV-----PLFWPLNSHFCTALVSLTHLFAFASVNTIVVSDRYLSIIHPLSYPSKWTQR 146

QY 148 M-LLILGASWLSLVGGIPILGNCLGHLE---ACSTVLPLYAKHYVLCVVTIFSIILL 203
DB 147 RGYLLYGTWIVAILQSTPLYGWGOAFDERNALCSMIWGASPSYTLISVFSVIVPLI 206

QY 204 AIVALVRIYCVVRSRSHA 221
DB 207 VMIACSVVFCARQHA 224

RESULT 14
US-10-627-633-2
/ Sequence 2, Application US/10627633
/ Publication No. US20050250720A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles, Andrew David
/ APPLICANT: Brennand, John Charles
/ APPLICANT: Hart, Kevin Anthony
/ TITLE OF INVENTION: Novel Compound
/ FILE REFERENCE: 1991-221
/ CURRENT APPLICATION NUMBER: US/10/627,633
/ CURRENT FILING DATE: 2003-07-28
/ PRIOR APPLICATION NUMBER: 09/722,342
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 60/172,146
/ PRIOR FILING DATE: 1999-12-17
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 415
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-627-633-2

Query Match          7.8%; Score 141; DB 6; Length 415;
Best Local Similarity 24.5%; Pred. No. 2.7e-05;
Matches 87; Conservative 54; Mismatches 128; Indels 86; Gaps 20;

QY 4 LYSEYL-----NPNKVQEHYNYKTETLETQSTTSRQVASAFITLCCAIWENLLV 54
DB 35 LPSQILMELSEHWSNQTDLHY-----VLKPGEVAT---ASIFPGILWLPSIFGNSLV 86
```

```
QY 55 LIAVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLLS-----GSVTLRTPVQWF 106
DB 87 CLVIHRSRRTQSTTNYFVVSMA CADLLISVASTPPVLLQFTTGRWTLGSATCKV--VRYP 144

QY 107 AREGSAFITLSASVFSLLAIAIERHVAIA-----KVLGYGDKSCRMLLLIGASWLI--S 159
DB 145 -----QYLTGPGQIYVLLSICIDREFYTIYVPLSFVSRKAKK-----MIAASWIFDAG 193

QY 160 LVLGGPLILGNCLGHLEACSTVLP-----LYAKHYVLCVVTIFSIILLAI---VALYV 210
DB 194 FVTPVLPFYGSWDSH---CNFLPSSWEGTAYTVIHFLVGVFIVSVLLILFYQVKIKYI 250

QY 211 -RIYCVVRSSHADM-AAPQT-LALLKTVTVILGVFIVCWLPAPFSILL-----DYACPV 261
DB 251 WRIGTDGRTVRRTNIVPRTKVKTKMFLILNLLFLLSWLP-FHVAQLMHPHEQDYK--- 306

QY 262 HSCPILYKAHYXFA-----VSTLNSLLNPVIYTWRSRDLRREV-----LRPLOCWR 307
DB 307 -----KSSLVFTAITWISFSSASKPTLYSIYNANFRGRMKETFCMSSMKCYR 354

RESULT 15
US-10-821-234-934
/ Sequence 934, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 934
/ LENGTH: 485
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-934

Query Match          7.8%; Score 140; DB 6; Length 485;
Best Local Similarity 21.9%; Pred. No. 3.9e-05;
Matches 62; Conservative 59; Mismatches 120; Indels 42; Gaps 11;

QY 51 NELLVIAVARNKSFHSAMYLFLGNLAASDLL--AGVAFVANTLLSGSVTLRLTPVQW-FA 107
DB 180 NIMAIWVILKMKVKKPAVVMHLATADLVFVSVLPFKISYVFGS-----DMQFG 231

QY 108 REGSAFIT-----LSASVFSLLAIAIERHVAIAKV-----KLYGDKSCRMLLLIGA 154
DB 232 SELCRFVTAAFYCNVVASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAIWALAI 291

QY 155 SWLISLVL--GGLPILGNCLGHLEACSTVL-----PLYAKHYVLCVVTIFSIILLAI 206
DB 292 AGVVPVLVLEQTIQVPGLN-----ITTCHDVNLNETLEGYYAYFSAFVFFVFPVLIIST 347

QY 207 ALYVRIYCVVRSSHADMAAPQTLALLKTVTVILGVFIVCWLPAPFSILLDDYACPVHSCPI 266
DB 348 VCYSIIRCLSSAVANRSKSRALFLSAA-VFCIFICFGTGNVLLIAHYFLSH-ST 405

QY 267 LYKAHYXF-----AVSTLNSLLNPVIYTWRSRDLRREVLRPLOC 305
DB 406 TEAAVFAVLLCVCSISSICIDPLIYYASSECQRYVYSILCC 448

Search completed: December 4, 2005, 06:42:26
Job time : 7 secs
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The Page with (1990)

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:23:06 ; Search time 115.5 Seconds
(without alignments)
1277.002 Million cell updates/sec

Title: US-10-084-507B-17
Perfect score: 1806
Sequence: 1 MGSLSYSEVLPNPKVQEHYNY.....LRCGMHPTPTFLRGNTVV 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------------------------|
| 1 | 1804 | 99.9 | 353 | 3 | US-09-771-063-2 Sequence 2, Appli |
| 2 | 1804 | 99.9 | 353 | 4 | US-10-084-507B-17 Sequence 17, Appl |
| 3 | 1803 | 99.8 | 353 | 3 | US-09-731-030A-19 Sequence 19, Appl |
| 4 | 1803 | 99.8 | 353 | 4 | US-10-084-507B-22 Sequence 22, Appl |
| 5 | 1787 | 98.9 | 353 | 3 | US-09-842-316-8 Sequence 8, Appli |
| 6 | 1787 | 98.9 | 353 | 3 | US-09-971-228-9 Sequence 9, Appli |
| 7 | 1787 | 98.9 | 353 | 3 | US-09-904-099-33 Sequence 33, Appl |
| 8 | 1787 | 98.9 | 353 | 4 | US-10-225-567A-508 Sequence 508, App |
| 9 | 1787 | 98.9 | 353 | 4 | US-10-228-762-19 Sequence 19, Appl |
| 10 | 1787 | 98.9 | 353 | 4 | US-10-393-870-3 Sequence 3, Appli |
| 11 | 1787 | 98.9 | 353 | 4 | US-10-421-828-8 Sequence 8, Appli |
| 12 | 1787 | 98.9 | 353 | 4 | US-10-715-117-7 Sequence 7, Appli |
| 13 | 1787 | 98.9 | 353 | 5 | US-10-498-848-46 Sequence 46, Appl |
| 14 | 1783 | 98.7 | 353 | 3 | US-09-771-063-4 Sequence 4, Appli |
| 15 | 1625.5 | 90.0 | 352 | 4 | US-10-084-507B-21 Sequence 21, Appl |
| 16 | 1432 | 79.3 | 372 | 3 | US-09-904-099-37 Sequence 37, Appl |
| 17 | 947 | 52.4 | 269 | 3 | US-09-764-886-47 Sequence 47, Appl |
| 18 | 947 | 52.4 | 269 | 3 | US-09-764-886-47 Sequence 47, Appl |
| 19 | 947 | 52.4 | 274 | 3 | US-09-764-886-74 Sequence 74, Appl |
| 20 | 947 | 52.4 | 274 | 3 | US-09-764-891-5338 Sequence 5338, Ap |
| 21 | 947 | 52.4 | 274 | 3 | US-09-764-886-74 Sequence 74, Appl |
| 22 | 860.5 | 47.6 | 384 | 3 | US-09-904-099-5 Sequence 5, Appli |
| 23 | 858.5 | 47.5 | 391 | 3 | US-09-904-099-3 Sequence 3, Appli |
| 24 | 858 | 47.5 | 362 | 3 | US-09-993-844-8 Sequence 8, Appli |
| 25 | 854.5 | 47.3 | 362 | 3 | US-09-993-844-8 Sequence 8, Appli |
| 26 | 854.5 | 47.3 | 362 | 4 | US-10-633-438-65 Sequence 65, Appl |
| 27 | 854.5 | 47.3 | 362 | 5 | US-10-901-772-65 Sequence 65, Appl |

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| 28 | 854.5 | 47.3 | 362 | 6 | US-11-026-435-8 Sequence 8, Appli |
| 29 | 849 | 47.0 | 341 | 3 | US-09-971-228-13 Sequence 13, Appl |
| 30 | 849 | 47.0 | 382 | 3 | US-09-971-228-5 Sequence 5, Appli |
| 31 | 849 | 47.0 | 382 | 3 | US-09-863-455-2 Sequence 2, Appli |
| 32 | 849 | 47.0 | 382 | 3 | US-09-759-514-2 Sequence 2, Appli |
| 33 | 849 | 47.0 | 382 | 3 | US-09-904-099-1 Sequence 1, Appli |
| 34 | 849 | 47.0 | 382 | 4 | US-10-087-192-786 Sequence 237, App |
| 35 | 849 | 47.0 | 382 | 4 | US-10-225-567A-237 Sequence 786, App |
| 36 | 849 | 47.0 | 382 | 4 | US-10-295-027-2 Sequence 2, Appli |
| 37 | 849 | 47.0 | 382 | 4 | US-10-429-160-72 Sequence 2, Appli |
| 38 | 849 | 47.0 | 382 | 4 | US-10-211-462-2 Sequence 2, Appli |
| 39 | 849 | 47.0 | 382 | 5 | US-10-491-545A-30 Sequence 30, Appl |
| 40 | 849 | 47.0 | 382 | 5 | US-10-498-848-38 Sequence 38, Appl |
| 41 | 849 | 47.0 | 448 | 4 | US-10-425-114-55760 Sequence 55760, A |
| 42 | 848 | 47.0 | 346 | 3 | US-09-971-228-15 Sequence 15, Appl |
| 43 | 847 | 46.9 | 383 | 6 | US-11-100-593-8 Sequence 8, Appli |
| 44 | 845 | 46.8 | 382 | 3 | US-09-969-711-2 Sequence 2, Appli |
| 45 | 845 | 46.8 | 382 | 4 | US-10-087-192-783 Sequence 783, App |

ALIGNMENTS

RESULT 1

US-09-771-063-2
; Sequence 2, Application US/09771063
; Patent No. US20010034331A1
; GENERAL INFORMATION:
; APPLICANT: Derek J. Bergsma
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Pamela Lane
; APPLICANT: Xiaotong Li
; APPLICANT: Jeffrey L. Mooney
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
; FILE REFERENCE: GP-70431-C1
; CURRENT APPLICATION NUMBER: US/09/771,063
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/150,650
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/082,776
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-771-063-2

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| Query Match | | 99.9%; | Score 1804; | DB 3; | Length 353; |
| Best Local Similarity | | 99.7%; | Pred. No. 2.7e-156; | | |
| Matches 352; | | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| QY | 1 | MGSLSYSEVLPNPKVQEHYNYK | ETLETTTSRQVASAFIVLCC | AI | VVENLLVLI |
| Db | 1 | MGSLSYSEVLPNPKVQEHYNYK | ETLETTTSRQVASAFIVLCC | AI | VVENLLVLI |
| QY | 61 | NSKFSHSMYFLGNLAASDLLAG | VAFVANTLLSGSVTLRLTP | VQWFA | REGSAPITLSASV |
| Db | 61 | NSKFSHSMYFLGNLAASDLLAG | VAFVANTLLSGSVTLRLTP | VQWFA | REGSAPITLSASV |
| QY | 121 | FSLLAIATERHVAIAKVKLYG | SKRCMLLLIGASWLSLV | LGGLPILG | MNCLGLEACS |
| Db | 121 | FSLLAIATERHVAIAKVKLYG | SKRCMLLLIGASWLSLV | LGGLPILG | MNCLGLEACS |
| QY | 181 | TVLPYAKHYLVCVVTIFSIIL | LAIVLVRYICVVRSSHAD | MAAPQTL | LALKTIVILG |
| Db | 181 | TVLPYAKHYLVCVVTIFSIIL | LAIVLVRYICVVRSSHAD | MAAPQTL | LALKTIVILG |
| QY | 241 | VFIVCWLPAFSLILLDYACP | HVSCPILYKAHYXFAV | STLNSLLN | PNVYTWRSRDLR |
| Db | 241 | VFIVCWLPAFSLILLDYACP | HVSCPILYKAHYXFAV | STLNSLLN | PNVYTWRSRDLR |

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Db |||||
301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSLERGHMPTSPTFLEGNVTW 353

RESULT 2
US-10-084-507B-17
; Sequence 17, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH
; APPLICANT: VIJAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084,507B
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (273)
; OTHER INFORMATION: Leu or Phe
US-10-084-507B-17

Query Match 99.9%; Score 1804; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.7e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLSYSEYNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
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QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATLSASV 120
Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATLSASV 120

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATLSASV 120
Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATLSASV 120

QY 121 FSLAIAIERHVAIAKVLKYGSKCRMLLIGASWLSLVGLGPIIGWNCGLGLEACS 180
Db |||||
121 FSLAIAIERHVAIAKVLKYGSKCRMLLIGASWLSLVGLGPIIGWNCGLGLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTTVILG 240
Db |||||
181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db |||||
241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSLERGHMPTSPTFLEGNVTW 353
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301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSLERGHMPTSPTFLEGNVTW 353

RESULT 3
US-09-731-030A-19
; Sequence 19, Application US/09731030A
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; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; CURRENT FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-19

Query Match 99.8%; Score 1803; DB 3; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.4e-156;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATLSASV 120

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Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATLSASV 120

QY 121 FSLAIAIERHVAIAKVLKYGSKCRMLLIGASWLSLVGLGPIIGWNCGLGLEACS 180
Db |||||
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181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
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241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSLERGHMPTSPTFLEGNVTW 353
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301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSLERGHMPTSPTFLEGNVTW 353

RESULT 4
US-10-084-507B-22
; Sequence 22, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH
; APPLICANT: VIJAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084,507B
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-507B-22

Query Match          99.8%; Score 1803; DB 4; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.4e-156;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLSYSEYLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAR 60
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DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120

QY 121 FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSISLVLGGLPILGWNCLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSISLVLGGLPILGWNCLHLEACS 180

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DB 181 TVPLPYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSRHADMAAPQTLALKTKTVIVLG 240

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DB 241 VFIWCLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGVQGRRRGTGPHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
DB 301 RPLQWRPGVGVQGRRRGTGPHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 5
US-09-842-316-8
; Sequence 8, Application US/09842316
; Patent No. US20020099191A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENSIS, Eva
; APPLICANT: GASSENHUBER, Johann
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
; FILE REFERENCE: 38005-147
; CURRENT APPLICATION NUMBER: US/09/842,316
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: EP 116589.3
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: EP 108858.2
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-316-8

Query Match          98.9%; Score 1787; DB 3; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MGSLSYSEYLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAR 60

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DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120

QY 121 FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSISLVLGGLPILGWNCLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSISLVLGGLPILGWNCLHLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSRHADMAAPQTLALKTKTVIVLG 240
DB 181 TVPLPYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSRHADMAAPQTLALKTKTVIVLG 240

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DB 241 VFIWCLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

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DB 301 RPLQWRPGVGVQGRRRGTGPHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 6
US-09-971-228-9
; Sequence 9, Application US/09971228
; Patent No. US20020155512A1
; GENERAL INFORMATION:
; APPLICANT: Liao, X. Charlene
; APPLICANT: Masuda, Eateban
; APPLICANT: Chu, Peter
; APPLICANT: Pardo, Joige
; APPLICANT: Li, Congfen
; APPLICANT: Zhao, Haoran
; APPLICANT: Jiang, Yingping
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
; FILE REFERENCE: 021044-000310US
; CURRENT APPLICATION NUMBER: US/09/971,228
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/284,763
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human endothelial differentiation G-protein
; OTHER INFORMATION: coupled receptor (GPCR) 5 (EDG5)
US-09-971-228-9

Query Match          98.9%; Score 1787; DB 3; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MGSLSYSEYLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120

QY 121 FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSISLVLGGLPILGWNCLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSISLVLGGLPILGWNCLHLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSRHADMAAPQTLALKTKTVIVLG 240
DB 181 TVPLPYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSRHADMAAPQTLALKTKTVIVLG 240

QY 241 VFIWCLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIWCLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGVQGRRRGTGPHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
DB 301 RPLQWRPGVGVQGRRRGTGPHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
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RESULT 7
US-09-904-099-33
; Sequence 33, Application US/09904099
; Publication No. US20030119092A1
; GENERAL INFORMATION:
; APPLICANT: Munning, Jason N
; APPLICANT: Spencer, Juliet V
; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 10602-013-999
; CURRENT APPLICATION NUMBER: US/09/904,099
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-099-33

Query Match      98.9%; Score 1787; DB 3; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKQVEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKQVEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAVFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAVFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Qy 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTIVLG 240
Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQCRPGVGVOGRRRGVTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVW 353
Db 301 RPLQCRPGVGVOGRRRGVTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVW 353

RESULT 8
US-10-225-567A-508
; Sequence 508, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 508
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-508

Query Match      98.9%; Score 1787; DB 3; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKQVEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKQVEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAVFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAVFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Qy 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTIVLG 240
Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQCRPGVGVOGRRRGVTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVW 353
Db 301 RPLQCRPGVGVOGRRRGVTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVW 353

RESULT 9
US-10-228-762-19
; Sequence 19, Application US/10228762
; Publication No. US20030130493A1
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Huang, Ling Yan
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Salton, John A.
; APPLICANT: Willson, Amy
; APPLICANT: Nagorny, Raisa
; TITLE OF INVENTION: DNA Encoding Edg7 Receptor
; FILE REFERENCE: 58230-a
; CURRENT APPLICATION NUMBER: US/10/228,762
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US/09/356,315
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 09/253,998
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-228-762-19

Query Match      98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKQVEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKQVEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAVFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAVFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Qy 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTIVLG 240
Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQCRPGVGVOGRRRGVTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVW 353
Db 301 RPLQCRPGVGVOGRRRGVTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVW 353
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QY 181 TVLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLLAKTIVVLG 240
Db 181 TVLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLLAKTIVVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQRRRGVTPGHLLPLRSSSSSLRGHMPPTSPTFLEGNVTV 353
Db 301 RPLQWRPGVGQRRRGVTPGHLLPLRSSSSSLRGHMPPTSPTFLEGNVTV 353

RESULT 10

US-10-393-870-3
; Sequence 3, Application US/10393870
; Publication No. US20030219808A1
; GENERAL INFORMATION:
; APPLICANT: KOZIAN, Detlef
; APPLICANT: KOSTENIS, Evi
; APPLICANT: SIELGER, Karl-Ernet
; APPLICANT: JACOBS, Martina
; APPLICANT: RICARD, Sylvain
; APPLICANT: MACE, Sandrine
; APPLICANT: DELEUZE, Jean-Francois
; TITLE OF INVENTION: ASSOCIATION OF EDG5 POLYMORPHISM WITH TYPE II DIABETES MELLITUS,
; TITLE OF INVENTION: VENOUS THROMBOSIS OR PULMONARY EMBOLISM AND THE USE THEREOF
; FILE REFERENCE: DEAV2002/0019 US NP
; CURRENT APPLICATION NUMBER: US/10/393,870
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-870-3

Query Match 98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNTKETLETTTSRQVASAFIVILCCAI VVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKVOEHYNTKETLETTTSRQVASAFIVILCCAI VVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
QY 181 TVLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLLAKTIVVLG 240
Db 181 TVLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLLAKTIVVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQRRRGVTPGHLLPLRSSSSSLRGHMPPTSPTFLEGNVTV 353
Db 301 RPLQWRPGVGQRRRGVTPGHLLPLRSSSSSLRGHMPPTSPTFLEGNVTV 353

RESULT 11

US-10-421-828-8
; Sequence 8, Application US/10421828
; Publication No. US20030219874A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIS, Eva

; APPLICANT: GASENHUBER, Johann
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
; FILE REFERENCE: 38005-147
; CURRENT APPLICATION NUMBER: US/10/421,828
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: EP 116589.3
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: EP 108858.2
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-421-828-8

Query Match 98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNTKETLETTTSRQVASAFIVILCCAI VVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKVOEHYNTKETLETTTSRQVASAFIVILCCAI VVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
QY 181 TVLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLLAKTIVVLG 240
Db 181 TVLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLLAKTIVVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQRRRGVTPGHLLPLRSSSSSLRGHMPPTSPTFLEGNVTV 353
Db 301 RPLQWRPGVGQRRRGVTPGHLLPLRSSSSSLRGHMPPTSPTFLEGNVTV 353

RESULT 12

US-10-715-117-7
; Sequence 7, Application US/10715117
; Publication No. US20040171037A1
; GENERAL INFORMATION:
; APPLICANT: LI, JING
; APPLICANT: POWERS, SCOTT
; APPLICANT: SIN, WUN CHEY
; APPLICANT: YANG, JIANKIN
; TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
; FILE REFERENCE: 38002-0062
; CURRENT APPLICATION NUMBER: US/10/715,117
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: 60/427,202
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/434,434
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-117-7

Query Match 98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;

Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLYSEYLNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAIVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAIVENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

Qy 121 FSLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSISLVGLGPLGNWNCGLGLEACS 180
Db 121 FSLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSISLVGLGPLGNWNCGLGLEACS 180

Qy 181 TVPLPYAKHYVLCVVTIFSIILLAIIVALYVRIYCVWRSSHADMAAPQTALLKTTVTVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAIIVALYVRIYCVWRSSHADMAAPQTALLKTTVTVLG 240

Qy 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

RESULT 13

US-10-498-848-46
; Sequence 46, Application US/10498848
; Publication No. US20050153289A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Method of Analyzing Gene Expression
; FILE REFERENCE: P02-0155PCT
; CURRENT APPLICATION NUMBER: US/10/498,848
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: JP 2001-382053
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: JP 2002-45104
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: JP 2002-140111
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: JP 2002-333769
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 46
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human
; US-10-498-848-46

Query Match 98.9%; Score 1787; DB 5; Length 353;
Best Local Similarity 99.2%; Pred. No. 9,8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 MGSLYSEYLNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAIVENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

Qy 121 FSLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSISLVGLGPLGNWNCGLGLEACS 180
Db 121 FSLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSISLVGLGPLGNWNCGLGLEACS 180

Qy 181 TVPLPYAKHYVLCVVTIFSIILLAIIVALYVRIYCVWRSSHADMAAPQTALLKTTVTVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAIIVALYVRIYCVWRSSHADMAAPQTALLKTTVTVLG 240

Qy 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300

Db 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

Db 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

RESULT 14

US-09-771-063-4
; Sequence 4, Application US/09771063
; Patent No. US20010034331A1
; GENERAL INFORMATION:
; APPLICANT: Derek J. Bergsma
; APPLICANT: Nabil Elsnourbagy
; APPLICANT: Pamela Lane
; APPLICANT: Xiaotong Li
; APPLICANT: Jeffrey L. Mooney
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
; FILE REFERENCE: GP-70431-C1
; CURRENT APPLICATION NUMBER: US/09/771,063
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/150,650
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/082,776
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-771-063-4

Query Match 98.7%; Score 1783; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 2.3e-154;
Matches 349; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGSLYSEYLNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAIVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAIVENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSISLVGLGPLGNWNCGLGLEACS 180
Db 121 FSLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSISLVGLGPLGNWNCGLGLEACS 180

Qy 181 TVPLPYAKHYVLCVVTIFSIILLAIIVALYVRIYCVWRSSHADMAAPQTALLKTTVTVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAIIVALYVRIYCVWRSSHADMAAPQTALLKTTVTVLG 240

Qy 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

RESULT 15

US-10-084-507B-21
; Sequence 21, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH

APPLICANT: VYAS, TEJAL B.
APPLICANT: GUPTA, ASHWANI K.
TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
FILE REFERENCE: 108074-00023
CURRENT APPLICATION NUMBER: US/10/084,507B
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/222,995
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/109,885
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/080,610
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/070,185
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 352
TYPE: PRT
ORGANISM: Rattus sp.
US-10-084-507B-21

Query Match 90.0%; Score 1625.5; DB 4; Length 352;
Best Local Similarity 89.8%; Pred. No. 5.6e-140;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

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DB 1 MGLSYEYLNPEKQVQEHYNYTKETLDMQETPSRKVASAFIILCCAIVVENLLVLIAR 60

QY 61 NGKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAFITLSASV 120
DB 61 NGKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSAFITLSASV 120

QY 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLICASWLIISLVGLGPLGWNCLHLEACS 180
DB 121 FSLIAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLIISLILGGLPILGWNCLHLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRYCVVRRSHADMAAPOTLALKTTIVILG 240
DB 181 TVLPLYAKHYVLCVVTIFSVILLAI VALYVRIYFVVRSSHADVAGPQTLLALKTTIVILG 240

QY 241 VFTVCWLPAPFILLLDYACPVHSCPTLYKAHYKFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFTICWLPAPFILLLDSTCFVRACPVLYKAHYFFAFATLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQCWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
DB 301 RPLLCWRQKGATG-RRGGNPGHRLPLRSSSSSLERGLHMTSPTFLEGNTVV 352

Search completed: December 4, 2005, 06:42:08
Job time : 117.5 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:10:25 ; Search time 33.5 Seconds
(without alignments)
871.180 Million cell updates/sec

Title: US-10-084-507B-17
Perfect score: 1806
Sequence: 1 MGSLEYLNKQVQHYNY.....LERGWHMPTPTFLEGNIVV 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/H COMB.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 1804 | 99.9 | 353 | 2 | US-09-582-200A-2 |
| 2 | 1804 | 99.9 | 353 | 2 | US-09-582-200A-5 |
| 3 | 1804 | 99.9 | 353 | 2 | US-09-582-200A-10 |
| 4 | 1803 | 99.8 | 353 | 2 | US-09-582-200A-4 |
| 5 | 1803 | 99.8 | 353 | 2 | US-09-582-200A-6 |
| 6 | 1803 | 99.8 | 353 | 2 | US-09-582-200A-12 |
| 7 | 1803 | 99.8 | 353 | 2 | US-09-731-030A-19 |
| 8 | 1760 | 97.5 | 353 | 2 | US-09-274-752D-3 |
| 9 | 1625.5 | 90.0 | 352 | 1 | US-08-196-989B-2 |
| 10 | 1625.5 | 90.0 | 352 | 1 | US-08-760-936-2 |
| 11 | 1625.5 | 90.0 | 352 | 2 | US-09-582-200A-11 |
| 12 | 1625.5 | 90.0 | 352 | 2 | US-09-169-205D-24 |
| 13 | 1625.5 | 90.0 | 352 | 2 | US-09-225-024-2 |
| 14 | 849 | 47.0 | 382 | 2 | US-09-262-477-2 |
| 15 | 847 | 46.9 | 383 | 1 | US-08-196-989B-4 |
| 16 | 847 | 46.9 | 383 | 1 | US-08-760-936-4 |
| 17 | 847 | 46.9 | 383 | 2 | US-09-225-024-4 |
| 18 | 845 | 46.8 | 382 | 2 | US-09-542-733-2 |
| 19 | 836.5 | 46.3 | 381 | 1 | US-08-845-566-3 |
| 20 | 836.5 | 46.3 | 381 | 1 | US-08-467-948A-28 |
| 21 | 836.5 | 46.3 | 381 | 2 | US-08-852-824-18 |
| 22 | 836.5 | 46.3 | 381 | 2 | US-08-467-947A-28 |
| 23 | 836.5 | 46.3 | 381 | 2 | US-09-731-030A-17 |
| 24 | 836.5 | 46.3 | 381 | 4 | PCT-US96-10618-4 |
| 25 | 836.5 | 46.3 | 381 | 4 | PCT-US96-10618-4 |
| 26 | 831 | 46.0 | 382 | 2 | US-09-169-205D-21 |
| 27 | 769 | 42.6 | 378 | 2 | US-09-082-088-2 |

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| 28 | 769 | 42.6 | 378 | 2 | US-09-546-117-2 | Sequence 2, Appli |
| 29 | 769 | 42.6 | 378 | 2 | US-09-169-205D-22 | Sequence 22, Appl |
| 30 | 769 | 42.6 | 378 | 2 | US-09-731-030A-18 | Sequence 18, Appl |
| 31 | 763 | 42.2 | 334 | 1 | US-08-118-270-73 | Sequence 73, Appl |
| 32 | 763 | 42.2 | 334 | 4 | PCT-US93-08528-73 | Sequence 73, Appl |
| 33 | 720.5 | 39.9 | 500 | 2 | US-09-875-076-30 | Sequence 30, Appl |
| 34 | 533 | 29.5 | 384 | 2 | US-09-731-030A-11 | Sequence 11, Appl |
| 35 | 529 | 29.3 | 384 | 2 | US-09-731-030A-13 | Sequence 13, Appl |
| 36 | 521 | 28.8 | 384 | 2 | US-08-852-824-4 | Sequence 4, Appli |
| 37 | 521 | 28.8 | 384 | 2 | US-09-518-383-4 | Sequence 4, Appli |
| 38 | 513 | 28.4 | 393 | 4 | PCT-US96-10618-3 | Sequence 3, Appli |
| 39 | 510 | 28.2 | 364 | 2 | US-09-169-205D-20 | Sequence 20, Appl |
| 40 | 509 | 28.2 | 364 | 2 | US-08-763-938-2 | Sequence 2, Appli |
| 41 | 507 | 28.1 | 364 | 4 | PCT-US96-10618-2 | Sequence 2, Appli |
| 42 | 504 | 27.9 | 364 | 2 | US-09-731-030A-15 | Sequence 15, Appl |
| 43 | 504 | 27.9 | 364 | 2 | US-09-811-838-2 | Sequence 2, Appli |
| 44 | 491 | 27.2 | 382 | 2 | US-09-169-205D-23 | Sequence 23, Appl |
| 45 | 491 | 27.2 | 382 | 2 | US-09-274-752D-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-09-582-200A-2
; Sequence 2, Application US/09582200A
; Patent No. 6482609

GENERAL INFORMATION:

; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: Unknown Xaa refers to any amino acid
US-09-582-200A-2

| | | | | | |
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| Query Match | | 99.9%; | Score 1804; | DB 2; | Length 353; |
| Best Local Similarity | | 100.0%; | Pred. No. 2.6e-146; | Mismatches 0; | Indels 0; Gaps 0; |
| Matches 353; | | Conservative | 0; | | |
| QY | 1 | MGSLEYLNKQVQHYNYTKETLETQETTSRQVASAFIVILCAIVVNLVLI | AVAR 60 | | |
| Db | 1 | MGSLEYLNKQVQHYNYTKETLETQETTSRQVASAFIVILCAIVVNLVLI | AVAR 60 | | |
| QY | 61 | NSKPHSAMYFLGNLAASDLAGVAVFVANTLLSGSVTLRLTPVQWFAREGS | AFITLSAV 120 | | |
| Db | 61 | NSKPHSAMYFLGNLAASDLAGVAVFVANTLLSGSVTLRLTPVQWFAREGS | AFITLSAV 120 | | |
| QY | 121 | FSLLAIAERHVAIAKVLYGSDKSRMLLLIGASWLSISLVLGGLPILGWNCL | GLEACS 180 | | |

Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGIPILGNCLGLEACS 180
Qy 181 TVLPYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Db 181 TVLPYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Qy 241 VFIVCWLPAFSAIILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSAIILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQWRPGVGVQGRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
Db 301 RPLQWRPGVGVQGRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

RESULT 2
US-09-582-200A-5
; Sequence 5, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyasa, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CONFLICT
; LOCATION: (272)..(274)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
US-09-582-200A-5

Query Match 99.9%; Score 1804; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.6e-146;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSLSYELNPNKVOEHYNTKETLEQTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYELNPNKVOEHYNTKETLEQTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGIPILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGIPILGNCLGLEACS 180

Qy 181 TVLPYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Db 181 TVLPYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Qy 241 VFIVCWLPAFSAIILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSAIILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQWRPGVGVQGRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
Db 301 RPLQWRPGVGVQGRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
RESULT 3
US-09-582-200A-10
; Sequence 10, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyasa, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human EDG-4 polypeptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: "Xaa" represents any amino acid
US-09-582-200A-10

Query Match 99.9%; Score 1804; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.6e-146;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSLSYELNPNKVOEHYNTKETLEQTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYELNPNKVOEHYNTKETLEQTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGIPILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGIPILGNCLGLEACS 180
Qy 181 TVLPYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Db 181 TVLPYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Qy 241 VFIVCWLPAFSAIILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSAIILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGMHMTSPPTFLEGNTVV 353
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Db 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGMHMTSPPTFLEGNTVV 353
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RESULT 4

US-09-582-200A-4
; Sequence 4, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-200A-4

Query Match 99.8%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAI VVENLLVLI AVAR 60
|||||
Db 1 MGSLYSEYNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAI VVENLLVLI AVAR 60
|||||
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
|||||
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
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QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
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Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
|||||
QY 181 TVPLYAKHYVLCVVTFISIIILAVVLYVRYCVVRS SHADMAAPQTALLKTTVIVLG 240
|||||
Db 181 TVPLYAKHYVLCVVTFISIIILAVVLYVRYCVVRS SHADMAAPQTALLKTTVIVLG 240
|||||
QY 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
|||||
Db 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
|||||
QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGMHMTSPPTFLEGNTVV 353
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Db 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGMHMTSPPTFLEGNTVV 353
|||||

RESULT 5

US-09-582-200A-6
; Sequence 6, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:

; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-200A-6

Query Match 99.8%; Score 1803; DB 2; Length 353;

Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAI VVENLLVLI AVAR 60
|||||
Db 1 MGSLYSEYNPNKQOEHNYYTKETLETQETTSRQVASAFIVILCCAI VVENLLVLI AVAR 60
|||||
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
|||||
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
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QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
|||||
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
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QY 181 TVPLYAKHYVLCVVTFISIIILAVVLYVRYCVVRS SHADMAAPQTALLKTTVIVLG 240
|||||
Db 181 TVPLYAKHYVLCVVTFISIIILAVVLYVRYCVVRS SHADMAAPQTALLKTTVIVLG 240
|||||
QY 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
|||||
Db 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
|||||
QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGMHMTSPPTFLEGNTVV 353
|||||
Db 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGMHMTSPPTFLEGNTVV 353
|||||

RESULT 6

US-09-582-200A-12
; Sequence 12, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY R+
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995

;
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human EDG-4 #36
US-09-582-200A-12

Query Match 99.8%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSLYSEYLNPNKQVQEHYNYTKETLEQTTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKQVQEHYNYTKETLEQTTTSROVASAFIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLHLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLHLEACS 180

Qy 181 TVPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTALLKTTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFISILLDYACPVHSCPILYKAHYXPAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

RESULT 7
US-09-731-030A-19
; Sequence 19, Application US/09731030A
; Patent No. 6566096
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; CURRENT FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-19

Query Match 99.8%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSLYSEYLNPNKQVQEHYNYTKETLEQTTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKQVQEHYNYTKETLEQTTTSROVASAFIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLHLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLHLEACS 180

Qy 181 TVPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTALLKTTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFISILLDYACPVHSCPILYKAHYXPAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

RESULT 8
US-09-274-752D-3
; Sequence 3, Application US/09274752D
; Patent No. 6812335
; GENERAL INFORMATION:
; APPLICANT: Goetzl, Edward L.
; APPLICANT: An, Songzhu
; TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipide and
; FILE REFERENCE: A-67501/DJB/TAL
; CURRENT APPLICATION NUMBER: US/09/274,752D
; CURRENT FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-274-752D-3

Query Match 97.5%; Score 1760; DB 2; Length 353;
Best Local Similarity 98.3%; Pred. No. 1.1e-142;
Matches 347; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MGSLYSEYLNPNKQVQEHYNYTKETLEQTTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKQVQEHYNYTKETLEQTTTSROVASAGIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLHLEACS 180
Db 121 GSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLHLEACS 180

Qy 181 TVPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTALLKTTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFISILLDYACPVHSCPILYKAHYXPAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353


```
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/592,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 352
; TYPE: PRT
; ORGANISM: rat EDG-4 polypeptide
US-09-582-200A-11

Query Match          90.0%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 4.6e-131;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSEYLNPNKVOEHYNYTKETLETQETTSRQVASFIVILCAIWNLLVLIIVAR 60
Db 1 MGSLYSEYLNPEKVOEHYNYTKETLDMQETPSRKVASAFIILCCAIWNLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLGPIILGNCLHLEACS 180
Db 121 FSLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSISLVGLGPIILGNCLHLEACS 180

Qy 181 TVLPLYAKHYVLCVVTIFSIILAIVALYVRIYCVVRSSHADMAAPQTLALLKTTVIVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSVIILAIVALYVRIYFVVRSSHADVAGPQTALLKTTVIVLG 240

Qy 241 VFIVCWLPAFSTLLLDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREV 300
Db 241 VFIIICWLPAPFSTLLDSTCPVRACPVLYKAHYFFAFATLNSLNPVIYTWRSRDLRREV 300

Qy 301 RPLOCWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVW 353
Db 301 RPLLCWRQKGATG-RRGNGPGRHLLPLRSSSSSLERGLHMTPTPTFLEGNTVW 352

RESULT 12
US-09-169-205D-24
; Sequence 24, Application US/09169205D
; Patent No. 6485922
; GENERAL INFORMATION:
; APPLICANT: Erikson, James
; APPLICANT: Goddard, J. Graham
; APPLICANT: Kiefer, Michael
; TITLE OF INVENTION: METHODS FOR DETECTING COMPOUNDS WHICH MODULATE THE
; TITLE OF INVENTION: ACTIVITY OF AN LPA RECEPTOR
; FILE REFERENCE: 252/004
; CURRENT APPLICATION NUMBER: US/09/169,205D
; CURRENT FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 24
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-169-205D-24

Query Match          90.0%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 4.6e-131;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSEYLNPNKVOEHYNYTKETLETQETTSRQVASFIVILCAIWNLLVLIIVAR 60
Db 1 MGSLYSEYLNPEKVOEHYNYTKETLDMQETPSRKVASAFIILCCAIWNLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLGPIILGNCLHLEACS 180
Db 121 FSLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSISLVGLGPIILGNCLHLEACS 180

Qy 181 TVLPLYAKHYVLCVVTIFSIILAIVALYVRIYCVVRSSHADMAAPQTLALLKTTVIVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSVIILAIVALYVRIYFVVRSSHADVAGPQTALLKTTVIVLG 240

Qy 241 VFIVCWLPAFSTLLLDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREV 300
Db 241 VFIIICWLPAPFSTLLDSTCPVRACPVLYKAHYFFAFATLNSLNPVIYTWRSRDLRREV 300

Qy 301 RPLOCWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVW 353
Db 301 RPLLCWRQKGATG-RRGNGPGRHLLPLRSSSSSLERGLHMTPTPTFLEGNTVW 352

RESULT 13
US-09-225-024-2
; Sequence 2, Application US/09225024
; Patent No. 6518414
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,024
; FILING DATE: 04-JAN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,936
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/196,989
; FILING DATE: 15-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
```


INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-225-024-2

Query Match 90.0%; Score 1625.5; DB 2; Length 352;

Best Local Similarity 89.8%; Pred. No. 4.6e-131;

Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

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QY 1 MGSLEYLNPKNKVOEHYNT-KETLETOETTSROVASAFIVILCCAIIVVENLLVIAVAR 60
DB 1 MGSLEYLNPKNKVOEHYNT-KETLETOETTSROVASAFIVILCCAIIVVENLLVIAVAR 60
QY 61 NSKFSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
DB 61 NSKFSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGDKSCRMMLLIGASWLSILVGLGPILGWNCGLHLEACS 180
DB 121 FSLAIAIERHVAIAKVKLYGDKSCRMMLLIGASWLSILVGLGPILGWNCGLHLEACS 180
QY 181 TVLPLVAKHYVLCVVTIFSIILAIIVAVLVRIYCVVRSMDMAAPQTLALLKTVTVLG 240
DB 181 TVLPLVAKHYVLCVVTIFSIILAIIVAVLVRIYCVVRSMDMAAPQTLALLKTVTVLG 240
QY 241 FVIVCWLPAFSLILLDYACPVHSCPTLYKAHYKFAVSTLNSLNPVITYWRSRLRREVL 300
DB 241 FVILCWLPAFSLILLDSTCPVACPVLYKAHYFAFATLSLNPVITYWRSRLRREVL 300
QY 301 RPLQWRPQGVQRRGTPGHLLPLRSSSSSLRGMMPTSPFLEGNTVV 353
DB 301 RPLLCWRQKGATG-RRGNPGHRLPLRSSSSSLRGHLMPTSPFLEGNTVV 352
```

RESULT 14

US-09-262-477-2

Sequence 2, Application US/09262477A

Patent No. 6423508

GENERAL INFORMATION:

APPLICANT: George Livi

APPLICANT: Derk Bergsma

APPLICANT: Jeffrey Stadel

APPLICANT: Winnie Chan

APPLICANT: Randall Johnson

APPLICANT: Shelagh Wilson

APPLICANT: Jon Chambers

APPLICANT: Philippe Robert

APPLICANT: Nassirah Khandoudi

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDE SEQUENCES OF HUMAN EDG-1C AND

TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND ANTAGONISTS FOR HUMAN

TITLE OF INVENTION: EDG-1C RECEPTOR AND SPHINGOSINE 1-PHOSPHATE LIGAND AND

TITLE OF INVENTION: INTERACTION THEREOF

FILE REFERENCE: GP50006

CURRENT APPLICATION NUMBER: US/09/262,477A

CURRENT FILING DATE: 1999-03-04

EARLIER APPLICATION NUMBER: 60/077,369

EARLIER FILING DATE: 1998-03-09

EARLIER APPLICATION NUMBER: 60/087,102

EARLIER FILING DATE: 1998-05-28

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 382

TYPE: PRT

ORGANISM: Human

US-09-262-477-2

Query Match 47.0%; Score 849; DB 2; Length 382;

Best Local Similarity 50.8%; Pred. No. 1.2e-64;

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Matches 160; Conservative 59; Mismatches 84; Indels 12; Gaps 2;
QY 3 SLYSEYLNPNKVOEHYNT-KETLETOETTSROVASAFIVILCCAIIVVENLLVIAVAR 61
DB 14 SSVSDYVNDIIVRHNTYTKLNISADRENSIKLTSVVFILCCFIILNIFVLTIWKT 73
QY 62 SKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 121
DB 74 KKFHRPMYFIGNLALS DLLAGVAVANTLLSGATYKLTTPAQWFLREGSMFVALSASF 133
QY 122 SLLAIAIERHVAIAKVKLYGDKSCRMMLLIGASWLSILVGLGPILGWNCGLHLEACS 181
DB 134 SLLAIAIERYITMLKMLHNGSNFRFLFLLISACWVISLILGGLPIMGWNCISALSSCST 193
QY 182 VLPLVAKHYVLCVVTIFSIILAIIVAVLVRIYCVVRS-----SHADMAAPQTLA 230
DB 194 VLPLVAKHYVLCVVTIFSIILAIIVAVLVRIYCVVRSRLTFRKNISKARSSEKSLA 253
QY 231 LLKTVTVILGVFIVCWLPAFSLILLDYACPVHSCPTLYKAHYKFAVSTLNSLNPVITYW 290
DB 254 LLKTVTVILSVFVFIACWAPLFIILLDVGKVKTCOILFRAEYFLVLAVLNSGTNPITL 313
QY 291 RSRDLRREVLRLPQC 305
DB 314 TNKEMRRAFIRIMSC 328
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RESULT 15

US-08-196-989B-4

Sequence 4, Application US/08196989B

Patent No. 5585476

GENERAL INFORMATION:

APPLICANT: MacLennan, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of

TITLE OF INVENTION: G-Protein Coupled Receptors

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/196,989B

FILING DATE: 15-FEB-1994

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lloyd, Jeff

REGISTRATION NUMBER: 35,589

REFERENCE/DOCKET NUMBER: MAC-100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-196-989B-4

Query Match 46.9%; Score 847; DB 1; Length 383;

Best Local Similarity 48.7%; Pred. No. 1.7e-64;

Matches 168; Conservative 60; Mismatches 103; Indels 14; Gaps 4;

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QY 3 SLYSEYLNPNKVOEHYNT-KETLETOETTSROVASAFIVILCCAIIVVENLLVIAVAR 61
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Db 15 SOVSDYGNVDIIVRHNYTKLNIGVEKDHGKLTSSVVFILICCLIIILENIFVLLTIWKT 74
Qy 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFPAREGSAFITLSASVF 121
Db 75 KKFHRPMYFFIGNLALSDDLAVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVF 134
Qy 122 SLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSISLVGGLPILGMNCLGHLEACST 181
Db 135 SLLAIAIERYITMLKKUHGNSRSRSELLISACWVISLIILGGUPIMGWNCISSLSGCST 194
Qy 182 VLPLYAKHYVLCVVTIFSGIILAIIVALYVRIYCVVRS-----SHADMAAPOTLA 230
Db 195 VLPLYKHYYILFCTTVFTLLLSIVILYCRYISLVRTSRRLTFRKNISKASRSSEKSLA 254
Qy 231 LLKTVTIVLGVPIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTW 290
Db 255 LLKTVIIVLSVFIACWAPLFILLILLDVGCKAKTCDILYKAHYFLVLAVINSGTNPVIYTL 314
Qy 291 RSRDLRREVLRPLQWR-PGVGVQGR-RRGGTPGHLLPLRSSSS 333
Db 315 TNKEMRRAFIRIISCCCKPNGDSAGKFKRPIIPGMFERSRSKSDNS 359

Search completed: December 4, 2005, 06:24:23
Job time : 35.5 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

...s Page Blank (usjio)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 06:38:02 ; Search time 152 seconds
(without alignments)
1638.497 Million cell updates/sec

Title: US-10-084-507B-17

Perfect score: 1806

Sequence: 1 MGSLEYLNPKNKQEHYNY.....LERGMHPTPTFLRGNTVV 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|--------|-------|--------|----|--------------|--------------------|
| 1 | 1804 | 99.9 | 353 | 1 | EDG5 HUMAN | O95136 homo sapien |
| 2 | 1631.5 | 90.3 | 352 | 2 | O8C3Q7_MOUSE | O8C3Q7 m mus muscu |
| 3 | 1625.5 | 90.0 | 352 | 1 | EDG5 RAT | P47752 rattus norv |
| 4 | 1625.5 | 90.0 | 352 | 2 | O54A16_RAT | O54A16 rattus norv |
| 5 | 1622.5 | 89.8 | 352 | 1 | EDG5 MOUSE | P52592 mus musculu |
| 6 | 998 | 55.3 | 370 | 1 | EDG5 BRARE | O918k8 brachydanio |
| 7 | 933 | 51.7 | 202 | 2 | O91XR0_CAVPO | O91XR0 cavia porce |
| 8 | 859 | 48.1 | 190 | 2 | O9ESK0_RAT | O9ESK0 rattus norv |
| 9 | 856 | 47.4 | 382 | 2 | Q5R7A1_PONPY | Q5R7A1 pongo pygma |
| 10 | 849 | 47.0 | 382 | 2 | O9NYN8_HUMAN | O9NYN8 homo sapien |
| 11 | 847 | 46.9 | 383 | 1 | EDG1 RAT | P48303 rattus norv |
| 12 | 847 | 46.9 | 383 | 2 | O4V7F6_RAT | O4V7F6 rattus norv |
| 13 | 845 | 46.8 | 382 | 2 | O9BC35_MOUSE | O9BC35 m mus muscu |
| 14 | 844 | 46.7 | 382 | 2 | O5B1P0_BOVIN | O5B1P0 bos taurus |
| 15 | 841 | 46.6 | 373 | 2 | O4T9E2_TETNG | O4T9E2 tetraodon n |
| 16 | 839 | 46.5 | 382 | 1 | EDG1 MOUSE | O08530 mus musculu |
| 17 | 837 | 46.3 | 375 | 2 | O5U389_BRARE | O5U389 brachydanio |
| 18 | 837 | 46.3 | 382 | 2 | O5E9P3_BOVIN | O5E9P3 bos taurus |
| 19 | 836.5 | 46.3 | 381 | 1 | EDG1 HUMAN | P21453 homo sapien |
| 20 | 835 | 46.2 | 374 | 2 | O6GLU6_XENLA | O6GLU6 xenopus lae |
| 21 | 822.5 | 45.5 | 326 | 2 | O99NR8_CASCN | O99NR8 castor cana |
| 22 | 820.5 | 45.4 | 325 | 2 | O71BN5_OTOGA | O71BN5 otolemur ga |
| 23 | 819 | 45.3 | 325 | 2 | O9BF55_ARTJA | O9BF55 artibeus ja |
| 24 | 817 | 45.2 | 362 | 1 | EDG1 BRARE | O9DDK4 brachydanio |
| 25 | 816.5 | 45.2 | 326 | 2 | O6JC76_9EUTH | O6JC76 solenodon p |
| 26 | 816.5 | 45.2 | 326 | 2 | O9BF73_CONCR | O9BF73 conylura c |
| 27 | 816.5 | 45.2 | 326 | 2 | O99NR0_HYSTB | O99NR0 cavia tscu |
| 28 | 816.5 | 45.2 | 326 | 2 | O99NR4_HYSBR | O99NR4 hystrix bra |
| 29 | 816 | 45.2 | 326 | 2 | O8MK87_TADBR | O8MK87 tadarda br |
| 30 | 815.5 | 45.2 | 326 | 2 | O99NQ7_AGOTA | O99NQ7 agouti tacz |
| 31 | 814 | 45.1 | 326 | 2 | O99NR1_HETGA | O99NR1 heteroceph |

| | | | | | | |
|----|-------|------|-----|---|--------------|--------------------|
| 32 | 813.5 | 45.0 | 326 | 2 | O9BF72_SORAR | O9BF72 sores arane |
| 33 | 813.5 | 45.0 | 326 | 2 | O99NQ9_HYDHY | O99NQ9 hydrochoeru |
| 34 | 813.5 | 45.0 | 326 | 2 | O99NR3_EREDY | O99NR3 erethizon d |
| 35 | 812.5 | 45.0 | 326 | 2 | O9BF75_MYRTR | O9BF75 myrmecophag |
| 36 | 812.5 | 45.0 | 326 | 2 | O9BF76_TAMTE | O9BF76 tamandua te |
| 37 | 811.5 | 44.9 | 326 | 2 | O9BF74_ERICO | O9BF74 erinaceus c |
| 38 | 811.5 | 44.9 | 326 | 2 | O9BF79_CHOHO | O9BF79 choloepus h |
| 39 | 811.5 | 44.9 | 326 | 2 | O99NR5_MOUSE | O99NR5 mus musculu |
| 40 | 811 | 44.9 | 292 | 2 | O91XR2_CAVPO | O91XR2 cavia porce |
| 41 | 809.5 | 44.8 | 325 | 2 | O99NR9_TAMST | O99NR9 tamias stri |
| 42 | 807.5 | 44.7 | 326 | 2 | O8MK86_MEGLY | O8MK86 megaderma l |
| 43 | 807.5 | 44.7 | 326 | 2 | O9BF66_ELEUR | O9BF66 elephantulu |
| 44 | 806.5 | 44.7 | 326 | 2 | O9BF65_ORYAF | O9BF65 orycteropus |
| 45 | 805.5 | 44.6 | 325 | 2 | O9BF41_PANON | O9BF41 panthera on |

ALIGNMENTS

RESULT 1
EDG5_HUMAN
ID EDG5_HUMAN STANDARD; PRT; 353 AA.
AC O95136; O8CUN8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
DE (Endothelial differentiation G-protein coupled receptor 5)
DE (Sphingosine 1-phosphate receptor 2) (S1P2).
GN Name=EDG5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;
RX PubMed=10617617; DOI=10.1074/jbc.275.1.288;
RA An S., Zheng Y., Bleu T.;
RT "Sphingosine 1-phosphate-induced cell proliferation, survival, and
RT related signaling events mediated by G protein-coupled receptors Edg3
RT and Edg5.";
RL J. Biol. Chem. 275:288-296(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Receptor for the lysosphingolipid sphingosine 1-
 CC phosphate (S1P). S1P is a bioactive lysophospholipid that elicits
 CC diverse physiological effect on most types of cells and tissues.
 CC When expressed in rat HTC4 hepatoma cells, is capable of mediating
 CC S1P-induced cell proliferation and suppression of apoptosis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF034780; AAC98919.1; -; mRNA.
 CC EMBL; AY262688; AAP20652.1; -; Genomic_DNA.
 CC EMBL; BC069598; AAH69598.1; -; mRNA.
 CC Ensembl; ENSG00000175898; Homo sapiens.
 CC HGNC; HGNC:3169; EDG5.
 CC MIM; 605111; .
 CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 CC GO; GO:0008289; F:lipid binding; TAS.
 CC GO; GO:000187; P:activation of MAPK; TAS.
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
 CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC InterPro; IPR004063; EDG5_receptor.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC InterPro; IPR004061; S1P_receptor.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR01525; EDG5RECEPTOR.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR01523; S1PRECEPTOR.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
 CC KW G-protein coupled receptor; Glycoprotein; Lipoprotein;
 CC Multigene family; Palmitate; Receptor; Transducer; Transmembrane.
 CC FT TOPO_DOM 1 34
 CC FT Transmem 35 59
 CC FT TOPO_DOM 60 66
 CC FT Transmem 67 95
 CC FT TOPO_DOM 96 109
 CC FT Transmem 110 128
 CC FT TOPO_DOM 129 147
 CC FT Transmem 148 173
 CC FT TOPO_DOM 174 189
 CC FT Transmem 190 210
 CC FT TOPO_DOM 211 233
 CC FT Transmem 234 255
 CC FT TOPO_DOM 256 271
 CC FT Transmem 272 292
 CC FT TOPO_DOM 293 305
 CC FT Lipid 305 305
 CC FT CARBOHYD 19 19
 CC FT CONFLICT 113 113 F -> S (in Ref. 1).
 CC FT CONFLICT 318 318 G -> V (in Ref. 1).
 CC SQ SEQUENCE 353 AA; 38867 MW; 8E37084284B7E8 CRC64;
 Query Match 99.9%; Score 1804; DB 1; Length 353;
 Best Local Similarity 99.7%; Pred. No. 1.8e-115;
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGSLYSYLNPKNVQEHYNTKETLETQTTSRQVASAFIVILCAIVENLLVLIAR 60
 Db 1 MGSLYSYLNPKNVQEHYNTKETLETQTTSRQVASAFIVILCAIVENLLVLIAR 60
 QY 61 NSKPHSAMVLFUNGLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFILTASV 120
 Db 61 NSKPHSAMVLFUNGLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFILTASV 120
 QY 121 FSLLAIAIERHVAIAKVLGYGDKSCRMILLIGASWLSLVLGGLPILGNWCLHLEACS 180
 Db 121 FSLLAIAIERHVAIAKVLGYGDKSCRMILLIGASWLSLVLGGLPILGNWCLHLEACS 180

QY 181 TVLPYAKHYVLCVVTIFSIILLAIYALYVRIYCVWRSSHADMAAPOTLALKTKTVILG 240
 Db 181 TVLPYAKHYVLCVVTIFSIILLAIYALYVRIYCVWRSSHADMAAPOTLALKTKTVILG 240
 QY 241 VFIVCWLPAFASILLDLAYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRLRREV 300
 Db 241 VFIVCWLPAFASILLDLAYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRLRREV 300
 QY 301 RPLQWRPGVGVQRRGGTGGHLLPLRSSSLRGMHMTPTSFLEGNTVV 353
 Db 301 RPLQWRPGVGVQRRGGTGGHLLPLRSSSLRGMHMTPTSFLEGNTVV 353
 RESULT 2
 Q8C3Q7_MOUSE
 ID Q8C3Q7_MOUSE PRELIMINARY; PRT; 352 AA.
 AC Q8C3Q7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
 DE library, clone:D430039A03 product:endothelial differentiation,
 DE sphingolipid G-protein-coupled receptor, 5, full insert sequence
 DE (Endothelial differentiation, sphingolipid G-protein-coupled receptor,
 DE 5).
 GN Name=Edg5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 FT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RX [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Washima J., Mazzairelli J., Wombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 FT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes."
RN Genome Res. 10:1617-1630(2000).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RN Genome Res. 10:1757-1771(2000).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Arawaka T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kusukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaga-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zengerg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBSJ databases.
CC -l- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AK085114; BAC39268.1; -; mRNA.
DR EMBL; BC096760; AAH96760.1; -; mRNA.
DR Ensembl; ENSMUSG00000043895; Mus musculus.
DR MGI; MGI:99569; Edg5.
DR GO; GO:0007610; P:behavior; IMP.
DR InterPro; IPR004063; EDG5 receptor.
DR InterPro; IPR000276; GPCR_Rhodpn.
DR InterPro; IPR004061; SLP_receptor.

DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; SLPRECEPTOR.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transducer; Transmembrane.
SQ SEQUENCE 352 AA; 38829 MW; 6A3E426B0FE54406 CRC64;
Query Match 90.3%; Score 1631.5; DB 2; Length 352;
Best Local Similarity 90.4%; Pred. No. 1.1e-103;
Matches 319; Conservative 12; Mismatches 21; Indels 1; Gaps 1;
QY 1 MGSLSYSEYNPNKQVHYNYTKETLETTSTSRQVASFIVILCAIVENLLVLIIVAR 60
DB 1 MGSLSYSEYNPNKQVHYNYTKETLETTSTSRQVASFIVILCAIVENLLVLIIVAR 60
QY 61 NSKFHSAWYFLGNLAASDLGAVAFVANTLLSGVTLRLTPVQWFAREGSAFILTASV 120
DB 61 NSKFHSAWYFLGNLAASDLGAVAFVANTLLSGVTLRLTPVQWFAREGSAFILTASV 120
QY 121 FSLAIAIAERHVAIAKVLGSKDSCRMILLIGASWLSLVGLLPILGWNCLGLEACS 180
DB 121 FSLAIAIAERHVAIAKVLGSKDSCRMILLIGASWLSLVGLLPILGWNCLGLEACS 180
QY 181 TVLPLVAKHYVLCVVTFISIIILAIYALYVRIYCVVRSHADMAAPOTLALLKTIVILG 240
DB 181 TVLPLVAKHYVLCVVTFISIIILAIYALYVRIYCVVRSHADMAAPOTLALLKTIVILG 240
QY 241 VFIICWLPAPFSLILLDSTCPVACPVLYKHYFAFATLNSLLNPNVITWRSRDLRREVL 300
DB 241 VFIICWLPAPFSLILLDSTCPVACPVLYKHYFAFATLNSLLNPNVITWRSRDLRREVL 300
QY 301 RPLQWRRGVGVQGRGGTGHLLPLRSSSLRGMHMTSPFTLSEGTNVV 353
DB 301 RPLQWRRGVGVQGRGGTGHLLPLRSSSLRGMHMTSPFTLSEGTNVV 352
RESULT 3
EDGS_RAT STANDARD; PRT; 352 AA.
AC P47752;
DT 01-FEB-1996 (Rel. 33, Created)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Spingosine 1-phosphate receptor Edg-5 (SLP receptor Edg-5) (G-protein
DE coupled receptor H218) (AGRI6) (Endothelial differentiation G-protein
DE coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (SLP2).
GN Name=Edg5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus;
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain, and Lung;
RX MEDLINE=94373324; PubMed=8087418; DOI=10.1006/mcne.1994.1024;
RA MacLennan A.J., Browe C.S., Gaskin A.A., Lado D.C., Shaw G.;
RT "Cloning and characterization of a putative G-protein coupled receptor
RT potentially involved in development."
RL Mol. Cell. Neurosci. 5:201-209(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aortic smooth muscle;
RX MEDLINE=93176155; PubMed=8382486;
RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
RA Takawa Y.;
RT "Molecular cloning of a novel putative G protein-coupled receptor
RT expressed in the cardiovascular system."
RL Biochem. Biophys. Res. Commun. 190:1104-1109(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;

RX MEDLINE=98072391; PubMed=9409733; DOI=10.1016/S0014-5793(97)01301-X;
RA An S., Bleu T., Huang W., Hallmark O.G., Coughlin S.R., Goetzl B.J.;
RT "Identification of cDNAs encoding two G protein-coupled receptors for
RL lysophospholipids."; *FEBS Lett.* 417:279-282 (1997).
RN [4]
RP PHARMACOLOGICAL CHARACTERIZATION.
RX PubMed=10383399; DOI=10.1074/jbc.274.27.18997;
RA Ancellin N., Hla T.;
RT "Differential pharmacological properties and signal transduction of
RT the sphingosine 1-phosphate receptors EDG-1, EDG-3, and EDG-5."; *J.
RL J. Biol. Chem.* 274:18997-19002 (1999).
CC -!- FUNCTION: Receptor for the lysophospholipid that elicits
CC phosphate (SIP). SIP is a bioactive lysophospholipid that elicits
CC diverse physiological effect on most types of cells and tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in all developing tissues with
CC highest levels detected in primitive, transformed cells. Relative
CC abundance: lung > kidney = skin > gut > spleen > brain > liver.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U10699; AA19241.1; -; mRNA.
DR EMBL; AF022138; AAC53494.1; -; mRNA.
DR PIR; JCI1465; JCI1465.
DR Ensembl; ENSRNOG0000020653; Rattus norvegicus.
DR RGD; 68334; Edg5
DR GO; GO:0004930; F:G-protein coupled receptor activity; IDA.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; SIP_receptor.
DR Pfam; PF00001; 7tm_1; 1_1_receptor.
DR PRINTS; PR01523; SIPRECEPTOR.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 34 Extracellular (Potential).
FT TRANSMEM 35 59 1 (Potential).
FT TOPO_DOM 60 66 Cytoplasmic (Potential).
FT TRANSMEM 67 95 2 (Potential).
FT TOPO_DOM 96 109 Extracellular (Potential).
FT TRANSMEM 110 128 3 (Potential).
FT TOPO_DOM 129 147 Cytoplasmic (Potential).
FT TRANSMEM 148 173 4 (Potential).
FT TOPO_DOM 174 189 Extracellular (Potential).
FT TRANSMEM 190 210 5 (Potential).
FT TOPO_DOM 211 233 Cytoplasmic (Potential).
FT TRANSMEM 234 255 6 (Potential).
FT TOPO_DOM 256 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT TOPO_DOM 293 352 Cytoplasmic (Potential).
FT LIPID 305 305 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 19 19 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 38735 MW; 9C933A18E756CE1E CRC64;

Query Match 90.0%; Score 1625.5; DB 1; Length 352;
Best Local Similarity 89.8%; Pred. No. 2.9e-103;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLYSEYLNPNKQVQEHYNYTKETLETOETTSRQVASFIVILCCAIWENLLVLIIVAR 60
DB 1 MGGLYSEYLNPNKQVQEHYNYTKETLETOETTSRQVASFIVILCCAIWENLLVLIIVAR 60
QY 61 NSKPHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120

Db 61 NSKPHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSKDCRMILIIIGASWLISLVGLPIGLWNCIGHLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSKDCRMILIIIGASWLISLVGLPIGLWNCIGHLEACS 180
QY 181 TVLPYAKHYVLCVVTTFISIIILAIIVLYVRIYCVVRSSHADMAAPOTLALKKTVTIVLG 240
Db 181 TVLPYAKHYVLCVVTTFISIIILAIIVLYVRIYCVVRSSHADVAGPQTALLKKTVTIVLG 240
QY 241 VFIYCWLPAPFISILLDYACPVHSCPIIYKHAHYXFAVSTLNSLLNPVIYTWRSRLRREV 300
Db 241 VFIICWLPAPFISILLDSTCPVACPVLYKHAHYFAFATLNSLLNPVIYTWRSRLRREV 300
QY 301 RPLQWPGVGVQGRRGCTPGHLLPLRSSSSLERGHMPTSTFLEGNTVV 353
Db 301 RPLLCWRQKGATG-RRGGNPGHLLPLRSSSSLERGLHMPSTPTFLEGNTVV 352
RESULT 4
Q54A16 RAT PRELIMINARY; PRT; 352 AA.
ID Q54A16 RAT PRELIMINARY; PRT; 352 AA.
AC Q54A16;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AGR16.
GN Name=AGR16;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
RX MEDLINE=93176155; PubMed=8382486;
RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
RA Takuwa Y.;
RT "Molecular cloning of a novel putative G protein-coupled receptor
RT expressed in the cardiovascular system";
RL Biochem. Biophys. Res. Commun. 190:1104-1109 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
RA Gonda K., Takuwa Y.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AB016931; BAA32454.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophospholipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; SIP_receptor.
DR Pfam; PF00001; 7tm_1; 1_1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL1; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 352 AA; 38735 MW; 9C933A18E756CE1E CRC64;

Query Match 90.0%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 2.9e-103;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLYSEYLNPNKQVQEHYNYTKETLETOETTSRQVASFIVILCCAIWENLLVLIIVAR 60
Db 1 MGGLYSEYLNPNKQVQEHYNYTKETLETOETTSRQVASFIVILCCAIWENLLVLIIVAR 60
QY 61 NSKPHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120

Db 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLOWFAREGSFATLSASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPIILGWNCLHLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPIILGWNCLHLEACS 180
Qy 181 TVPLKYAHYVLCVVTIFSIILLAI VALVRYICVVRSSHADVAAPOTLALKKTIVTVLG 240
Db 181 TVPLKYAHYVLCVVTIFSVILLAI VALVRYICVVRSSHADVAGPOTLALKKTIVTVLG 240
Qy 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKHAHYKFAVSTLNSLLNPVYIYWRSDLRREVL 300
Db 241 VFIIICWLPAFSLILLDSTCPVRACPVLYKHAHYFFAFATLNSLLNPVYIYWRSDLRREVL 300
Qy 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSSSLRGMMPTSPFLEGNVV 353
Db 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSSSLRGMMPTSPFLEGNVV 352

RESULT 5

EDG5_MOUSE STANDARD; PRT; 352 AA.
AC P52532; Q9R236;
DT 01-OCT-1996 (Rel. 34, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
DE (lysophospholipid receptor B2) (Endothelial differentiation G-protein coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2).
GN Names=Edg5; Synonyms=Gpcr13, Lpb2;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RC STRAIN=129/SvJ;
RX MEDLINE=9913230; PubMed=9931453; DOI=10.1016/S0378-1119(98)00589-7;
RA Zhang G., Contos J.J.A., Weiner J.A., Fukushima N., Chun J.;
RT "Comparative analysis of three murine G-protein coupled receptors activated by sphingosine-1-phosphate.";
RL Gene 227:89-99(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 62-241.
RC TISSUE=Testis;
RX MEDLINE=94116980; PubMed=8288218;
RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
RA Copeland N.G., Jenkins N.A.;
RT "Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptors.";
RL Genomics 18:175-184(1993).

CC -1- FUNCTION: Receptor for the lysophingolipid sphingosine 1-phosphate (S1P). S1P is a bioactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Most abundant in heart and lung; low, but clearly observed in kidney, liver and thymus; much lower but detectable in brain, testis, stomach and intestine. Not significantly detected in any of the sections of embryonic day (E) 14-18, except in embryonic brain.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC ENBL; AF108020; AAD16976.1; -; Genomic_DNA.
CC ENBL; L20334; AAL16846.1; -; mRNA.
CC PIR; E48909; E48909.
CC Ensembl; ENSMUSG00000043895; Mus musculus.
CC -----

DR MGI; 99569; Edg5.
DR GO; 0007610; P:behavior; IMP.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; S1P_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 34 Extracellular (Potential).
FT TRANSMEM 35 59 1 (Potential).
FT TOPO_DOM 60 66 Cytoplasmic (Potential).
FT TRANSMEM 67 95 2 (Potential).
FT TOPO_DOM 96 109 Extracellular (Potential).
FT TRANSMEM 110 128 3 (Potential).
FT TOPO_DOM 129 147 Cytoplasmic (Potential).
FT TRANSMEM 148 173 4 (Potential).
FT TOPO_DOM 174 189 Extracellular (Potential).
FT TRANSMEM 190 210 5 (Potential).
FT TOPO_DOM 211 233 Cytoplasmic (Potential).
FT TRANSMEM 234 255 6 (Potential).
FT TOPO_DOM 256 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT TOPO_DOM 293 305 Cytoplasmic (Potential).
FT LIPID 305 305 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 19 19 N-linked (GlcNAc...) (Potential).
FT CONFLICT 166 166 P -> S (in Ref. 2).
FT CONFLICT 175 175 Q -> K (in Ref. 2).
FT CONFLICT 189 189 H -> R (in Ref. 2).
SQ SEQUENCE 352 AA; 38871 MW; 9A3E456DD488FE6B CRC64;
Query Match 89.8%; Score 1622.5; DB 1; Length 352;
Best Local Similarity 90.1%; Pred. No. 4.6e-103;
Matches 318; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLSEYLNPNKQVHEHYNTKETLETQSTTSQVASFIVILCCAIYVENLLVIAVAR 60
Db 1 MGGLSEYLNPNKQVHEHYNTKETLDMQETTSKVASAFIILCCAIYVENLLVIAVAR 60
Qy 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATLSASV 120
Db 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGHVTLRLTPVQWFAREGSFATLSASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPIILGWNCLHLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPIILGWNCLHLEACS 180
Qy 181 TVPLKYAHYVLCVVTIFSIILLAI VALVRYICVVRSSHADVAAPOTLALKKTIVTVLG 240
Db 181 TVPLKYAHYVLCVVTIFSVILLAI VALVRYICVVRSSHADVAGPOTLALKKTIVTVLG 240
Qy 241 VFIVCWLPAFSLILLDYACPVHSCPTLYKHAHYKFAVSTLNSLLNPVYIYWRSDLRREVL 300
Db 241 VFIIICWLPAFSLILLDSTCPVRACPVLYKHAHYFFAFATLNSLLNPVYIYWRSDLRREVL 300
Qy 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSSSLRGMMPTSPFLEGNVV 353
Db 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSSSLRGMMPTSPFLEGNVV 352

RESULT 6

EDG5_BRARE STANDARD; PRT; 370 AA.
ID EDG5_BRARE
AC Q91878;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
DE (Sphingosine 1-phosphate receptor 2) (S1P2).

GN Name=edg5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS MIL HIS-150 AND CYS-167.
RX MEDLINE=20365730; PubMed=10910360; DOI=10.1038/35018092;
RA Kupperman E., An S., Osborne N., Waldron S., Stainier D.Y.R.;
RT "A sphingosine-1-phosphate receptor regulates cell migration during
vertebrate heart development.";
RL Nature 406:192-195 (2000).
CC -!- FUNCTION: Receptor for the lysophingolipid sphingosine 1-
phosphate (S1P). S1P receptor is critical for cell migration and
epithelial integrity during vertebrate embryogenesis.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: The expression pattern is complex and
dynamic. Maternal expression is found in a diffuse pattern
throughout the blastoderm, and this pattern persists through the
onset of gastrulation. More pronounced expression can be seen at
tailbud stage in the anterior portion of the embryo and along the
midbrain/hindbrain boundary and the tip of the tail where blisters
later develop in receptor mutants. At the 18-somite stage,
expression appears just lateral to the midline, and as the
myocardial precursors migrate to the midline, their location
overlaps with this domain of receptor expression.
CC -!- DISEASE: Defects in edg5 are a cause of heart development
abnormality named miles apart (mil). In all vertebrates, the
myocardial progenitors involute early during gastrulation and come
to occupy bilateral positions in the anterior lateral plate
mesoderm (lpm). During somitogenesis, these cells undergo a second
phase of migration toward the midline and fuse to form the
definitive heart tube. Defects in EDG5 disrupt this process,
leading to the formation of two laterally positioned hearts
(cardia bifida). The mil phenotype for which two recessive alleles
exist, mil(m93) and mil(te273) are fully penetrant.
CC Mil(m93)/mil(te273) transheterozygous embryos display the same
phenotype as homozygotes for either single mutant allele. In
addition to cardia bifida, mil mutants display epithelial tail
blisters, indicative of a defect in epithelial integrity.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; AF260256; AAF88001.1; -; mRNA.
CC Ensembl; ENSDARG00000009719; Danio rerio.
CC ZFIN; ZDB-GENE-020123-2; edg5.
CC InterPro; IPR000987; EDG1receptor.
CC InterPro; IPR000276; GPCR Rhodopsin.
CC InterPro; IPR004061; S1P_receptor.
CC Pfam; PF00001; 7cm1; 1.
CC PRINTS; PR00642; EDG1RECEPTOR.
CC PRINTS; PR00237; GPCR RHODOPSIN.
CC PRINTS; PR01523; S1PRECEPTOR.
CC PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
KW Disease mutation; G-protein coupled receptor; Glycoprotein;
Lipoprotein; Palmitate; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 57 Extracellular (Potential).
FT TRANSMEM 58 78 1 (Potential).
FT TOPO_DOM 79 87 Cytoplasmic (Potential).
FT TRANSMEM 88 108 2 (Potential).
FT TOPO_DOM 109 128 Extracellular (Potential).
FT TRANSMEM 129 149 3 (Potential).
FT TOPO_DOM 150 167 Cytoplasmic (Potential).
FT TRANSMEM 168 188 4 (Potential).
FT TOPO_DOM 189 214 Extracellular (Potential).

FT TRANSMEM 215 235 5 (Potential).
FT TOPO_DOM 236 254 Cytoplasmic (Potential).
FT TRANSMEM 255 275 6 (Potential).
FT TOPO_DOM 276 289 Extracellular (Potential).
FT TRANSMEM 290 310 7 (Potential).
FT TOPO_DOM 311 370 Cytoplasmic (Potential).
FT LIPID 325 325 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 24 24 N-linked (GlcNAc...) (Potential).
FT VARIANT 167 167 R -> H (in mil; allele m93; lack of
mediated signaling).
FT VARIANT 167 167 R -> C (in mil; allele te273; lack of
S1P-mediated signaling).
SQ SEQUENCE 370 AA; 41777 MW; 8C6B3A06DEEA6757 CRC64;
Query Match 55.3%; Score 998; DB 1; Length 370;
Best Local Similarity 58.5%; Pred. No. 2.4e-60;
Matches 200; Conservative 51; Mismatches 73; Indels 18; Gaps 4;
QY 3 SLYSEYLNPNKVQEHVNYTKE-----TLETQETTSRQVASFIVILCCAIUVENLLV 54
DB 17 SKYQYFNKTLQVHYLTAKETAEELRDRIKSSQJSS--LNILFVVICIIILENLLV 74
QY 55 LIAVARNSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFI 114
DB 75 LIAVFRNKKFSAFFIGNLAFSDLLAGSAYIANIFLSGRTFHLTPVQWFIREGTAFI 134
QY 115 TLSASVSFLLAIAIERHVAIAKVLYGSDKSCRMLLIGASWLISLVGLGPILGWNCIG 174
DB 135 ALSASVSFLLAIAIERVIAITKVYGSNKTCTRMFLITGACWMSILGGLPIIGWNCIN 194
QY 175 HLEACSTVLPYAKHYVLCVVTIFSIITLLAVALVYRYCVVRSASHADMAAPQTLALLKT 234
DB 195 NLDDCSAVLPUNTRYIRFVVTFISILLSIVLYRYLIVRTSHQATNSPAVALLKT 254
QY 235 VTIVGLVFVFCWLPFAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLNLNPIVYTWRSRD 294
DB 255 VTIVGLVFVFCWLPFAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLNLNPIVYTWRSRD 314
QY 295 LRREVLRLPQCRPGVGVQRRRGTPGHH-LLPIRSSSSSLE 335
DB 315 MRKEFLRLCCW-----GLLNCGRPPHRCWVPLKSSSSME 349
RESULT 7
Q91XR0_CAVPO PRELIMINARY; PRT; 202 AA.
AC Q91XR0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endothelial differentiation sphingolipid G-protein-coupled receptor 5
DE (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=hartley; TISSUE=Myenteric plexus;
RA Segura B.J., Xiao L., Cowles R.A., Turner D.J., Logsdon C.D.,
RA Mulholland M.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289992; AAK83087.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophingolipid and lysophosphatidic acid . . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR004061; S1P_receptor.
DR Pfam; PF00001; 7cm1; 1.

| | | | |
|----|-------------------------------------------------------------------|----------------------------------------------------|--|
| | DR | PRINTS; PRO1525; EDG5RECEPTOR. | |
| | DR | PRINTS; PRO0237; GPCRHHODOPSN. | |
| | DR | PRINTS; PRO1523; S1PRECEPTOR. | |
| | DR | PROSITE; PS00237; G_PROTEIN_RECEP_Fl_1; UNKNOWN-1. | |
| | DR | PROSITE; PS0262; G_PROTEIN_RECEP_Fl_2; 1. | |
| KW | G-protein coupled receptor; Receptor; transducer; Transmembrane. | | |
| FT | NON_TER 1 202 202 | | |
| SQ | SEQUENCE 202 AA; 21836 MW; D9814EC85B42320A CRC64; | | |
| | Query Match | 51.7%; Score 933; DB 2; Length 202; | |
| | Best Local Similarity | 91.6%; Pred. No. 3.8e-56; | |
| | Matches 185; Conservative | 9; Mismatches 8; Indels 0; Gaps 0; | |
| QY | 20 YTKETLETQTTSRQVASAFIVLCCAIIVENLVLIAVARNSKFHSAMVLFIGNLAASD | 79 | |
| Dd | 1 YTKETLDVRETTRSQVASAFIVLCCAIIVENLVLVAGRNKLSHSMVLFIGNLAASD | 60 | |
| QY | 80 LLAGVAFAVANTLLSGSVTLRLTPQWFAREGSAPITLSASFSLILAIATERHVATAKVKL | 139 | |
| Dd | 61 LLAGVAFTAINTLLSGSVTLQLTPVEWAREGSAPITLSASFVSILLAIAIERHVATAKVKL | 120 | |
| QY | 140 YGSDKSCKRMILLIGASWLISVLGGLPILGWNCGLGLEACSTVPLPYAKHYVLCVVWTIFS | 199 | |
| Dd | 121 YGSDKSCKRMILLIGASWYLIVLGGLPIWGNCIGLRDTGTCTVPLPYAQKYVLCVVWTIFS | 180 | |
| QY | 200 IILLAAIVALVRIYCVRSSHA 221 | | |
| Dd | 181 VILLAAIVLVRIYCVRSSHA 202 | | |

| | |
|------------|---------------------------------------------------------------------------|
| RESULT | 8 |
| Q9ESKO_RAT | PRELIMINARY; PRT; 190 AA. |
| ID | Q9ESKO_RAT |
| AC | Q9ESKO; |
| DT | 01-MAR-2001 (TrEMBLrel. 16, Created) |
| DT | 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) |
| DT | 01-OCT-2003 (TrEMBLrel..25, Last annotation update) |
| DE | Putative G-protein coupled receptor (Fragment). |
| DE | Name=GPCR18; |
| OS | Rattus norvegicus (Rat). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; |
| OC | Muridae; Murinae; Rattus. |
| OX | NCBI_TaxID=10116; |
| RN | [1] |
| RP | NUCLEOTIDE SEQUENCE. |
| RC | SFRAIN=Sprague-Dawley/Hsd; |
| RA | Carroll S.L., Miller M.L., Benedict-Hamilton H.M.; |
| RL | Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. |
| DR | EMBL; AF090995; AAG24259.1; -; mRNA. |
| DR | GO; GO:0016021; C:integral to membrane; IEA. |
| DR | GO; GO:0001619; F:lysophingolipid and lysophosphatidic acid . . ; IEA. |
| DR | GO; GO:0004872; F:receptor activity; IEA. |
| DR | GO; GO:0007186; F:g-protein coupled receptor protein signalin. . . ; IEA. |
| DR | GO; GO:0007165; P:signal transduction; IEA. |
| DR | InterPro; IPR004063; EDG5_receptor. |
| DR | InterPro; IPR000276; GPCR_Rhodpsn. |
| DR | InterPro; IPR004061; s1p_receptor. |
| DR | Pfam; PF00001; 7cm1; 1. |
| DR | PRINTS; PR01525; EDG5RECEPTOR. |
| DR | PRINTS; PR00237; GPCRRHODOPSN. |
| DR | PRINTS; PR01523; SIPRECEPTOR. |
| DR | PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1. |
| KW | G-protein coupled receptor; Receptor; Transducer; Transmembrane. |
| FT | NON_TER 1 |
| FT | NON_TER 190 |
| FT | SEQUENCE 190 AA; 20718 MW; 3CA0A5C188E168B1 CRC64; |

Query Match 48.1%; Score 869; DB 2; Length 190;
Best Local Similarity 88.9%; Pred. No. 8.6e-52;
Matches 169; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

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RESULT 9
QSR7A1_PONPY
ID QSR7A1_PONPY PRELIMINARY; PET; 382 AA.
QSR7A1;
AC 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469M1119.
GN Name=DKFZp469M1119;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (Nov-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; CR60217; CA923359.1; -; mRNA.
DR GO; GO:0016031; C: integral to membrane; IEA.
DR GO; GO:0001619; F: lysophospholipid and lysophosphatidic acid . . . ; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR000987; EDG1receptor.
DR InterPro; IPR002277; EDG2_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; Slp_receptor.
DR PANTHER; PTHR19266:SF5; EDG1receptor; 1.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00642; EDG1RECEPTOR.
DR PRINTS; PR01148; EDG2RECEPTOR.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01523; SI-RECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RCCEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RCCEP_F1_2; 1.
DR KW G-protein coupled receptor; Hypothetical protein; Receptor;
DR Transducer; Transmembrane.
SQ SEQUENCE 382 AA: 42773 MW: 6F0841D0E93789CC CRC64;

```

[illegible]

QY 122 SLTAIAIERHVAIAKVLGSKSCRMILLIGASWLSILVGLGPIILGNCGLHLEACST 181
 Db 134 SLTAIAIERHVAIAKVLGSKSCRMILLIGASWLSILVGLGPIILGNCGLHLEACST 193
 QY 182 VLPLAKHYVLCVVTTFISIIILAIIVLVYRIYCVVRS-----SHADMAAPOTLA 230
 Db 194 VLPLAKHYVLCVVTTFISIIILAIIVLVYRIYCVVRS-----SHADMAAPOTLA 253
 QY 231 LLKTTVTVLGVFIVCWLPAFSLILLLDYPACPVHSCPILYKAHYXFAVSTLSLNPVIYTW 290
 Db 254 LLKTTVTVLGVFIVCWLPAFSLILLLDYPACPVHSCPILYKAHYXFAVSTLSLNPVIYTW 313
 QY 291 RSRDLRREVLRLPLOC 305
 Db 314 TNKEMRRAFIRIMSC 328

RESULT 10
 ID Q5YN8 HUMAN PRELIMINARY; PRT; 382 AA.
 AC Q5YN8; Q5Y4;
 DT 01-OCT-2000 (TremBLrel. 15, Created)
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
 DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
 DE G protein-coupled sphingolipid receptor (Edg1 protein) (Endothelial
 DE differentiation, sphingolipid G-protein-coupled receptor, 1).
 GN Name=CHEDG1; Synonyms=EDG1; ORFNames=RP4-575N6.1-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RA Tiyi G.J. Sr., Wang D. Sr.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]

NUCLEOTIDE SEQUENCE.

RP TISSUE=Lung;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]

NUCLEOTIDE SEQUENCE.

RP TISSUE=Lung;
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]

NUCLEOTIDE SEQUENCE.

RA Halleck A., Ebert L., Mkontinya M., Schick M., Eisenstein S.,
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., Labaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [5]

NUCLEOTIDE SEQUENCE.

RP Grahnam D.;
 RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; AF233365; AAF43420.1; -; mRNA.
 DR EMBL; BC018650; AAH18650.1; -; mRNA.
 DR EMBL; CR541786; CAG46585.1; -; mRNA.
 DR EMBL; CR542259; CAG7065.1; -; mRNA.
 DR EMBL; AL109741; CAI21861.1; -; Genomic DNA.
 DR Ensembl; ENSG00000170989; Homo sapiens.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001619; F:lysophingolipid and lysophosphatidic acid . . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000987; EDG1receptor.
 DR InterPro; IPR002277; EDG2 receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR004061; S1P_receptor.
 DR PANTHER; PTHR19266:SF5; EDG1receptor; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00642; EDG1RECEPTOR.
 DR PRINTS; PR01148; EDG2RECEPTOR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PRINTS; PR01523; S1PRECEPTOR.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; UNKNOWN_1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 382 AA; 42811 MW; 0CCE8685A5E1BAD2 CRC64;

Query Match 47.0%; Score 849; DB 2; Length 382;

Best Local Similarity 50.8%; Pred. No. 3.9e-50;

Matches 160; Conservative 59; Mismatches 84; Indels 12; Gaps 2;

QY 3 SLYSEYLNPNKVOEHNYT-KETLETOBTSQVASFIVILCCAIIVVENLLVLIIVARN 61
 Db 14 SSVSDYVNDYDIIVRHNYTGLNISADKENSIKLTSVVFILICCFILLENIFVLLTIWKT 73
 QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASVF 121
 Db 74 KKFHRPMYFIFGNLSDLLAGVAVTANLLSGATVTKLTTPAQWFLREGSMFVALSASFV 133
 QY 122 SLTAIAIERHVAIAKVLGSKSCRMILLIGASWLSILVGLGPIILGNCGLHLEACST 181
 Db 134 SLTAIAIERHVAIAKVLGSKSCRMILLIGASWLSILVGLGPIILGNCGLHLEACST 193
 QY 182 VLPLAKHYVLCVVTTFISIIILAIIVLVYRIYCVVRS-----SHADMAAPOTLA 230
 Db 194 VLPLAKHYVLCVVTTFISIIILAIIVLVYRIYCVVRS-----SHADMAAPOTLA 253
 QY 231 LLKTTVTVLGVFIVCWLPAFSLILLLDYPACPVHSCPILYKAHYXFAVSTLSLNPVIYTW 290
 Db 254 LLKTTVTVLGVFIVCWLPAFSLILLLDYPACPVHSCPILYKAHYXFAVSTLSLNPVIYTW 313
 QY 291 RSRDLRREVLRLPLOC 305
 Db 314 TNKEMRRAFIRIMSC 328

RESULT 11

EDG1_RAT
 ID EDG1_RAT
 AC P48303;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Sphingosine 1-phosphate receptor Edg-1 (Sphingosine 1-phosphate
 DE receptor 1) (S1P).
 GN Name=Edg1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:38:17 ; Search time 24.5 Seconds
(without alignments)
1386.307 Million cell updates/sec

Title: US-10-084-507B-17
Perfect score: 1806
Sequence: 1 MGSLYSEYLNPNKQEHYNY.....LERGMHMTPTFLEGNTVV 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------|--------------------|
| 1 | 1625.5 | 90.0 | 352 | JC1465 | probable G protein |
| 2 | 847 | 46.9 | 383 | I53870 | Edg-1 orphan recep |
| 3 | 836.5 | 46.3 | 381 | A35300 | G protein-coupled |
| 4 | 817.5 | 45.3 | 362 | JC7559 | sphingosine 1-phos |
| 5 | 809 | 44.8 | 180 | E48909 | G protein-coupled |
| 6 | 769 | 42.6 | 378 | JC5245 | G protein-coupled |
| 7 | 504 | 27.9 | 364 | JC5293 | lysophosphatidic a |
| 8 | 352.5 | 19.5 | 323 | S43850 | melanocortin 3 rec |
| 9 | 349 | 19.3 | 362 | I65990 | G protein-coupled |
| 10 | 348.5 | 19.3 | 360 | B46647 | melanocortin recep |
| 11 | 347 | 19.2 | 330 | A55689 | G protein-coupled |
| 12 | 340.5 | 18.9 | 363 | S48697 | probable G protein |
| 13 | 338.5 | 18.7 | 223 | S36636 | melanocortin recep |
| 14 | 338 | 18.7 | 330 | S40454 | G protein-coupled |
| 15 | 302 | 16.7 | 473 | A33117 | cannabinoid recep |
| 16 | 300 | 16.6 | 325 | JC2193 | melanocortin recep |
| 17 | 298.5 | 16.5 | 332 | A57055 | melanocortin recep |
| 18 | 297 | 16.4 | 372 | I49008 | melanocortin-5 rec |
| 19 | 296.5 | 16.4 | 314 | S71420 | melanocortin 1 rec |
| 20 | 296.5 | 16.4 | 325 | JC2552 | melanocortin 5 rec |
| 21 | 292.5 | 16.2 | 325 | JN0764 | melanocortin recep |
| 22 | 292.5 | 16.2 | 347 | S70364 | cannabinoid recep |
| 23 | 288 | 15.9 | 472 | S17595 | cannabinoid recep |
| 24 | 286 | 15.8 | 360 | S36750 | cannabinoid recep |
| 25 | 285.5 | 15.8 | 412 | A48978 | adenosine receptor |
| 26 | 285 | 15.8 | 317 | S45708 | adenosine receptor |
| 27 | 283.5 | 15.7 | 314 | S70005 | adenosine receptor |
| 28 | 283 | 15.7 | 410 | A48974 | adenosine receptor |
| 29 | 281.5 | 15.6 | 320 | S18444 | G protein-coupled |

ALIGNMENTS

RESULT 1

JC1465
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JC1465
R:Okazaki, H.; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takuwa, Y
Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993
A:Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in t
A:Reference number: JC1465; MUID:93176155; PMID:8382486
A:Accession: JC1465
A:Molecule type: mRNA
A:Residues: 1-352 <OKA>
A:Cross-references: UNIPROT:P47752; UNIPARC:UPI000000007D; GB:AB016931; NID:g3445557; PI

A:Experimental source: aortic smooth muscle
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:35-59/Domain: transmembrane #status predicted <TM1>
F:67-95/Domain: transmembrane #status predicted <TM2>
F:110-128/Domain: transmembrane #status predicted <TM3>
F:148-173/Domain: transmembrane #status predicted <TM4>
F:190-210/Domain: transmembrane #status predicted <TM5>
F:234-255/Domain: transmembrane #status predicted <TM6>
F:272-293/Domain: transmembrane #status predicted <TM7>
F:19/Binding site: carboxylate (Asn) (covalent) #status predicted
F:142,145,218,219,329,330,331,332/Binding site: phosphate (Ser) (covalent) #status predi
F:313/Binding site: phosphate (Thr) (covalent) #status predicted

| | | | | |
|-----------------------|-----------------|--------------------------------------------------------------|----------|------------|
| Query Match | 90.0% | Score 1625.5 | DB 2 | Length 352 |
| Best Local Similarity | 89.8% | Pred. No. 1.5e-125 | | |
| Matches 317 | Conservative 13 | Mismatches 22 | Indels 1 | Gaps 1 |
| QY | 1 | MGSLYSEYLNPNKQEHYNYKTLETQETTSRQVASAFIVILCAIVVENLLVLIAVAR | 60 | |
| Db | 1 | MGSLYSEYLNPNKQEHYNYKTLETQETTSRQVASAFIVILCAIVVENLLVLIAVAR | 60 | |
| QY | 61 | NSKFSHANYLFLGNLAASDLLAGVAVFANTLLSGSVTLRLTPVQMFAREGSAFILTASV | 120 | |
| Db | 61 | NSKFSHANYLFLGNLAASDLLAGVAVFANTLLSGSVTLRLTPVQMFAREGSAFILTASV | 120 | |
| QY | 121 | FSLLAIATERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGLPILGWNCLHLEACS | 180 | |
| Db | 121 | FSLLAIATERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGLPILGWNCLHLEACS | 180 | |
| QY | 181 | TVLPYAKHYVLGVVTFISFIILAIVALYVRIYCVVRRSHADMAAPQTLALKTTIVILG | 240 | |
| Db | 181 | TVLPYAKHYVLGVVTFISFIILAIVALYVRIYCVVRRSHADMAAPQTLALKTTIVILG | 240 | |
| QY | 241 | VFIVCWLPAFSILLIDYACPVHSCPILYKAKHYKFAVSTLNSLLNPVIYTWRSRDRLREV | 300 | |
| Db | 241 | VFIVCWLPAFSILLIDYACPVHSCPILYKAKHYKFAVSTLNSLLNPVIYTWRSRDRLREV | 300 | |

| | | | | | | | | | | | | | | | |
|-----------------------------------------|-----|--------------|-------|--------|--------|-----|-----|-------|------|-----|-----|-------|------|------|-----|
| Qy | 127 | AIERHVAIAKVL | YGS | DKSCRM | LLIGAS | WLI | SLV | GLPIL | GWNC | LGH | EAC | STV | LP | LY | 186 |
| | | | : | | : | | : | | : | | : | | : | | |
| Db | 133 | AIERHLLTWI | KMR | PPYD | ANK | RHR | VFL | LIG | MCL | IAF | TLG | ALPIL | GWNC | LHNL | PCD |
| | | | : | | : | | : | | : | | : | | : | | 192 |
| Qy | 187 | AKHVLCW | VTIFS | ILL | AI | VAL | VYR | YCV | RVSS | HAD | MA | --- | AP | OT | L |
| | | | : | | : | | : | | : | | : | | : | | 242 |
| Db | 193 | SKKYI | ARC | S | I | F | T | A | I | L | V | I | Y | A | I |
| | | | : | | : | | : | | : | | : | | : | | 252 |
| Qy | 243 | I | V | C | W | L | P | A | S | F | I | L | L | D | Y |
| | | | : | | : | | : | | : | | : | | : | | 302 |
| Db | 253 | I | A | C | S | P | L | F | I | L | D | V | A | C | R |
| | | | : | | : | | : | | : | | : | | : | | 311 |
| Qy | 303 | L | Q | C | R | P | G | V | G | V | Q | R | R | G | T |
| | | | : | | : | | : | | : | | : | | : | | 341 |
| Db | 312 | L | V | C | --- | N | C | L | V | R | G | R | G | A | S |
| | | | : | | : | | : | | : | | : | | : | | 349 |
| RESULT 7 | | | | | | | | | | | | | | | |
| JCS293 | | | | | | | | | | | | | | | |
| lyso phosphatidic acid receptor - human | | | | | | | | | | | | | | | |
| N;Alternate names: Edg2 protein | | | | | | | | | | | | | | | |
| C;Species: Homo sapiens (man) | | | | | | | | | | | | | | | |

C;Accession: J05293
C;Title: Molecular cloning of the human Edg2 protein and its identification as
A;Reference number: J05293; MUID:97224397; PMID:9070858
A;Contents: lung
A;Accession: J05293
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-364 <NA>
A;Cross-references: UNIPROT:Q92633; UNIPARC:UPI0000050403; GB:U80811; NID:g185
C;Superfamily: G protein-coupled receptor edg-1

Query Match 27.9%; Score 504; DB 2; Length 364;
Best Local Similarity 34.3%; Pred. No. 8.6e-34;

| | | | |
|----|-----|---------------------------------------------------------------|-----|
| Qy | 18 | YNYTKETLEQTQETTSRQVASAFIVILCAIYVENLLVLIAVARNSKFHSAMTYLFIGNLAA | 77 |
| Db | 34 | YNRSCKHLATEWNTVSKLVMGLGTVCIFIMLANLLVMVAIYVNRFRFFPIYFLMANLAA | 93 |
| Qy | 78 | SDLLAGVAFVANTLLSGSVTLRLTPQVFAREGSAFITLSASVFSLAIAIATRHVAIAKV | 137 |
| Db | 94 | ADFFAGLAIYFVLMENGTGNTRLTVSTWLLRQGLDITSLTASVANLLAIAIERHITVFRM | 153 |
| Qy | 138 | KLYGSDKSCRMLLIGASWLITSLVLGGLPILGWNCGLHLEACSTVLPYAKHYVLCVVPI | 197 |
| Db | 154 | QLHTRMSNRVVVIVITWTAIVMGALPSPGVWNCICDIENCSNMAPLYSDSY-LVFWAI | 212 |
| Qy | 198 | FSII-LLAIYALVYRIYCVWR-----SSHADMAAPQ-----TLALLTKVTIVLGVFIVC | 245 |
| Db | 213 | FNLVTEVVMVVLIAHIFGYVRQRTWMSRHS--SGPRNRNRTMMSLLKTTVIVLGAFIIC | 270 |
| Qy | 246 | WLPAFSTILLDYACPVISCPILYKAHYFAVSTLNSLLNPVITYWRSDDLREVLRLPLOC | 305 |
| Db | 271 | WTPGLVILLDLVCCPF--QCDVLAYEKFFLLLAEFNSAMNPITYSYRDKEMSATFQRIICC | 328 |

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QY 306 WRPGVGQGRKKQGI FGNHMLFLRKSQSSJEA-----GTH 335
      ||| |||
Db 329 QR-----SENPTGTSSD-----RSASLNHTILAGVH 357
      ||| |||

RESULT 8
S43850
melanocortin 3 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43850; S37153
R:Desarnaud, F.; Labbe, O.; Eggerickx, D.; Vassart, G.; Parmentier, M.

```

```
RESULT 8
S43850
melanocortin 3 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jan-1995 #sequence_revision
C:Accession: S43850; S37153
R:Desarnaud, F.; Labbe, O.; Eggerickx,
```

Biochem. J. 299, 367-373, 1994
A:Title: Molecular cloning, functional expression and pharmacological characterization of
A:Reference number: S43850, MUID:94226597, PMID:8172596
A:Accession: S43850
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <DEG>
A:Cross-references: UNIPROT:P33033; UNIPARC:UPI0000004010; EMBL:X74983; NID:g400473; PIDN
C:Superfamily: melanocortin receptor

Query Match 19.5%; Score 352.5; DB 2; Length 323;
Best Local Similarity 34.0%; Pred. No. 1.9e-21;
Matches 98; Conservative 52; Mismatches 93; Indels 45; Gaps 11;
QY 41 VILCCAIV--VENLLVLIIVARNKSFHSAVYFLGNLAASDLLAGVAVANTLL-----S 93
DB 44 VFLALGIVSLMENILVILAVRNGNLHSPYFFFLCSLAADMLVSLNSLETIMIAVINS 103
QY 94 GSVTLRTPVQWFAR--EGSAFILTASVFSLLAIAIERHVAIAKVLYGSKSCR-MLL 150
DB 104 DSLTELDQFIQMDNIFSMTCISLVASICNLLAIAIDRYVTIFVALRYHHSIMTVRKALT 163
QY 151 LIGASWLSLVGLGPIILGNWCLHLEACSTVPLV--AKHYVLCVVTTFISIIILIAIVAL 208
DB 164 LIGVIWV-----CCG---ICGVWFIIYSESXWIVVCLITWFFAMVLLMGTL 206
QY 209 YVRYCVVR-----SSHADMAAPQTLALK---TWTIVLGVFIVCWLPAFSLILLDY 257
DB 207 YIHMFLFARLHVQRIAVLPAGVAPQOHSQWKGAVTITLLGVFPCWAPFFLHLVLI 266
QY 258 ACPVHSCPILYKAHY--XFAVSTLNSLNPVYTWRSRDLR---REV 300
DB 267 TCPTNPYCYTAHNTVILVLMCNSVIDPLIYAFRSLELRNTFKBIL 314

RESULT 9
165990
G protein-coupled receptor 6 - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
A:Accession: I65990
R:Heiber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, A.
DNA Cell Biol. 14, 25-35, 1995
A:Title: Isolation of three novel human genes encoding G protein-coupled receptors.
A:Reference number: 153033; MUID:95134353; PMID:7832990
A:Accession: I65990
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <RES>
A:Cross-references: UNIPROT:P46095; UNIPARC:UPI000000DA4A; GB:I36150; NID:g598156; PIDN:
C:Genetics:
A:Gene: GDB:GPR6
A:Cross-references: GDB:371713; OMIM:600553
A:Map position: 6q21-6q21
C:Superfamily: melanocortin receptor

Query Match 19.3%; Score 349; DB 2; Length 362;
Best Local Similarity 34.1%; Pred. No. 4.1e-21;
Matches 101; Conservative 53; Mismatches 106; Indels 36; Gaps 13;
QY 41 VILCCA---IVVENLLVLIIVARNKSFHSAVYFLGNLAASDLLAGVAVANTLL---LSG 94
DB 77 VLLCVSGTVIAGENALVVALIASTPALRTPMFLVGLSLATADLLAGCGLLILHFVQVLVP 136
QY 95 SVTLRLTPVQWFARFAGSAPILTASVFSLLAIAIERHVAIAKVLYGSKSCR-CEMLLLIG 153
DB 137 SETVSLTV-----GFLVASFASVSSLLAITVDRIYLSUNALTYYSRRLLGVHLLLA 190
QY 154 ASWLSLVGLGPIILGNWCLHLEACSTVPLVYKAHYVLCVVTTFISIIILIAIVALYRIY 213
DB 191 ATWTVSLGLGLLPVLGNWCLAEAAACSVVRPLARSHVALLSAAPFMVFGI-MLHLVYRI- 248
QY 214 CVVRSSHAD-----MAAQTLALK---TWTIVLGVFIVCWLPAFSLILLDYACPV- 261

Db 249 CQVVRHAHQIALQOHCILAPHLAATKGVCTLAVLGTFCASWLP-FAIY-----CVVG 302
QY 262 -HSCPILYKAHYXFAVSTLNSLNPVYTWRSRDLRREV-LRPLOQWRPVGVOGR 315
DB 303 SHEDPAVY-TVATLLPATYNSMINPIIYAFRNOIQIRALWLLLCGCCFQSKVPFRSR 357

RESULT 10
B46647
melanocortin receptor 3 - human
C:Species: Homo sapiens (man)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998
A:Accession: B46647
R:Gantz, I.; Konda, Y.; Tashiro, T.; Shimoto, Y.; Miwa, H.; Munzert, G.; Watson, S.J.;
J. Biol. Chem. 268, 8246-8250, 1993
A:Title: Molecular cloning of a novel melanocortin receptor.
A:Reference number: A46647; MUID:93216807; PMID:8463333
A:Accession: B46647
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-360 <GAN>
A:Cross-references: UNIPARC:UPI00001789CB
A:Note: sequence extracted from NCBI backbone (NCBIP:129161)
C:Genetics:
A:Gene: GDB:MC3R
A:Cross-references: GDB:138780
A:Map position: 20q13.2-20q13.3
C:Superfamily: melanocortin receptor

Query Match 19.3%; Score 348.5; DB 2; Length 360;
Best Local Similarity 33.4%; Pred. No. 4.5e-21;
Matches 102; Conservative 49; Mismatches 101; Indels 53; Gaps 12;
QY 32 SRQVASAFI-----VILCCAIV--VENLLVLIIVARNKSFHSAVYFLGNLAASDLL 81
DB 64 SNQSSAFCEQVFKPEIFLSGLIVSLENTLVILAVRNGNLHSPYFFFLCSLAVADML 123
QY 82 AGVAFVANTLL-----SGSVTLRLTPVQWFAR--EGSAFILTASVFSLLAIAIERHVAI 134
DB 124 VSVSNALETIMIAIIVSDDVTFFDQFIQMDNIFDSMICISLVASIGNLLAIAVDRYVTI 183
QY 135 AKVLYGSKSCR-MLLIGASWLSVPLVGLGPIILGNWCLHLEACSTVPLV--AKHYV 191
DB 184 FYALRYHSIMTVRKALTLIVAIWV-----CCG---VGVVVFIVYSESXWVI 226
QY 192 LCVVTIFSIIILIAIVALYVRIYCVVR-----SSHADMAAPQTLALK---TWTIVLG 240
DB 227 VCLITWFFAMLLMGTLIVHMFLEARLHVKRIALPADGVAPQOHSQWKGAVTITLLG 286
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHY--XFAVSTLNSLNPVYTWRSRDLR-- 296
DB 287 VFIFCWAPFFLHLVLIITCPTNPYCTCTAHTNTVILVLMCNSVIDPLIYAFRSLELRNT 346
QY 297 -REV 300
DB 347 FREIL 351

RESULT 11
A55689
G protein-coupled receptor 3 - human
N:Alternate names: G protein-coupled receptor GPR3; orphan G-protein-coupled receptor AC
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
A:Accession: A55689; S58521; G55733
R:Ilsmad, T.P.; Klefer, J.; Liu, M.L.; Baker, E.; Sutherland, G.R.; Shine, J.
Genomics 24, 391-394, 1994
A:Title: Isolation and chromosomal localization of a novel human G-protein-coupled recep
A:Reference number: A55689; MUID:95213036; PMID:7698767
A:Accession: A55689
A:Status: preliminary
A:Molecule type: DNA; mRNA

A;Residues: 1-330 <IIS>
A;Cross-references: UNIPROT:P46089; UNIPARC:UPI0000001624; GB:L32830; GB:L32831; NID:960
R;Eggerickx, D.; Denef, J.F.; Labbe, O.; Hayashi, Y.; Refetoff, S.; Vassart, G.; Parmant
Blochem. J. 309, 837-843, 1995
A;Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutively a
A;Reference number: S58521; MUID:95366960; PMID:7639700
A;Accession: S58521
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-330 <EG>
A;Cross-references: UNIPARC:UPI0000001624; GB:X83956; NID:g1061125; PIDN:CAA58787.1; PID
R;Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, H.H.Q.; Tsui, I
Genomics 23, 609-618, 1994
A;Title: Cloning of human genes encoding novel G protein-coupled receptors.
A;Reference number: A55733; MUID:95154831; PMID:7851889
A;Accession: C55733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-292 <MAR>
A;Cross-references: UNIPARC:UPI000016A113; GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:
C;Genetics:
A;Gene: GDB:GPR3
A;Cross-references: GDB:371695; OMIM:600241
A;Map position: lp36.1-lp34.3
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.2%; Score 347; DB 2; Length 330;
Best Local Similarity 33.3%; Pred. No. 5.4e-21;
Matches 96; Conservative 49; Mismatches 107; Indels 36; Gaps 11;

Qy 38 AFIVILCCA---IVVENLILVAVARNKSFHSAMYLFLGNLAASDLLAGVAFV---ANTL 91
Db 42 AMDVVLICSGTLVSCENALVAVIIVGTAPAPMELLVGLSLAVADLLAGLGLVLFHFAVF 101

Qy 92 LSGSVTLRLTPVQWFAREGAFITLSASFVSLALAIERHVAIAKVLKYGSDKS-CRMLL 150
Db 102 CIGSAEMSLV-----GVLAWAFASIGSLAITVDRLSLYNALTYSETTVTRYV 155

Qy 151 LIGASNLISLVGLGPIILGNWCLHLEACSTVPLVYAKHYLCVVTIISI--ILLAIVAL 208
Db 156 MLALVWGGALGLGLPLVLANWCLDGLTTCGVVYPLSKNHLVLAIAFFWFGIMQLYQA 215

Qy 209 YRIYCVVRSSHADMAAPQTLAL-----LKTIVILGVFIVCWLPAFSLILLDY 257
Db 216 ICRIVC-----RHAQQTALQRHLLPASHYVATRKGIATLAVLGAFAACWLPTVYCLGD 271

Qy 258 ACPVHSCPIYKAHYKFAVSTLNSLNPVIYTWRSRDLRREVLRLPQC 305
Db 272 A--HS-PPLY-TYATLLPATYNSMINPIIYAFRNQVQK-VLWAVCC 313

RESULT 12
S48697
probable G protein-coupled receptor protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S48697
R;Song, Z.H.; Young III, W.S.; Brownstein, M.J.; Bonner, T.I.
FEBS Lett. 351, 375-379, 1994
A;Title: Molecular cloning of a novel candidate G protein-coupled receptor from rat brain
A;Reference number: S48697; MUID:94364507; PMID:8082799
A;Accession: S48697
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <SON>
A;Cross-references: UNIPROT:P51651; UNIPARC:UPI000012BA34; EMBL:U12006; NID:g551333; PID
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor

Query Match 18.9%; Score 340.5; DB 2; Length 363;
Best Local Similarity 34.7%; Pred. No. 2e-20;
Matches 96; Conservative 51; Mismatches 95; Indels 35; Gaps 12;

Qy 41 VILCCA---IVVENLILVAVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLLS---G 94
Db 78 VLLCSGVTVIAGENALVVALIASTPALRTPMFLVGLSATADLLAGCGLLHFVQYVVP 137

Qy 95 SVTURLTPVQWFAREGAFITLSASFVSLALAIERHVAIAKVLKYGSDKS-CRMLLIG 153
Db 138 SETVSLLMV-----GFLVASFAASVSLAITVDRLSLYNALTYYSRRITLLGVHLLLA 191

Qy 154 ASWLISLVGLGPIILGNWCLHLEACSTVPLVYAKHYLCVVTIISIILLAIVALYVRIY 213
Db 192 ATWTVSLGLGLPLVIGWNCCLADRASCVVRELTSHVAL--LSTSFVVGIMLHLVRI- 249

Qy 214 CVWRSSHAD-----MAAPQTLALK---TVTIVLGVFIVCWLPAFSLIILLDYACPVH 262
Db 250 QOVVWRHAHQIALQOHCILAPPHLAATRKVGVTAAVLGTFCASMLP-PAIY-----CVVG 303

Qy 263 S--CPILYKAHYKFAVSTLNSLNPVIYTWRSRDLRR 297
Db 304 SQEDPAIY-TYATLLPATYNSMINPIIYAFRNQEIQR 339

RESULT 13
S36636
melanocortin receptor 3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A48254; S36636
R;Roselli-Rehftuss, L.; Mounjoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatro, J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8856-8860, 1993
A;Title: Identification of a receptor for gamma melanotropin and other proopiomelanocort
A;Reference number: A48254; MUID:94022273; PMID:8415620
A;Accession: A48254
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-323 <ROS>
A;Cross-references: UNIPROT:P32244; UNIPARC:UPI000012ED4C; EMBL:X70667; NID:g396551; PID
A;Note: submitted to the EMBL Data Library, January 1993
A;Note: in Genbank entry RMC3RA, release 113.0, the source is designated as Rattus ratt
C;Genetics:
A;Gene: MC3-R
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.7%; Score 338.5; DB 2; Length 323;
Best Local Similarity 32.1%; Pred. No. 2.6e-20;
Matches 95; Conservative 56; Mismatches 104; Indels 41; Gaps 11;

Qy 41 VILCCAIV--VENLILVAVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLL-----S 93
Db 44 VFLALGIVSLMENTILVILAVVRNGNLHSPMYFFLLSLQADMVLSLSNLETIMIVINS 103

Qy 94 GSVTURLTPVQWFA--EGSAFITLSASFVSLALAIERHVAIAKVLKYGSDKSCRMILL 151
Db 104 DSLTLEDQFIQHMDFDSMICISILVASICNLLAIAVDRIYVTFYALRYHSHMTVRKAL- 162

Qy 152 IGASNLISLVGLGPIILGNWCLHLEACSTVPLV--AKHYLCVVTIISIILLAIVALY 209
Db 163 ---SLIVAI-----WVCCG---ICGVMPFIVYSEKMWIVLCUITMFFAFWMLMGTY 207

Qy 210 VRIYCVWR-----SSHADMAAPQTLALAK---TVTIVLGVFIVCWLPAFSLIILLDYA 258
Db 208 IHMFLFARLHVQRIALPAPDGVAPQOHCKMGAVTIILLGVFFICFWAPFHLHLVLIIT 267

Qy 259 CPVHSCPIYKAHY--XPAVSTLNSLNPVIYTWRSRDLRREVLRLPQCWRGVGV 312
Db 268 CPTNFCYCYTAHFNTYLVLMCNVIDPLIYAFRSLEL-RNTFKELLCGCGMNV 322

RESULT 14
S40454
G protein-coupled receptor GPCR21 - mouse
C;Species: Mus musculus (house mouse)

C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S40454
R;Saeki, Y.; Ueno, S.; Mizuno, R.; Nishimura, T.; Fujimura, H.; Nagai, Y.; Yanagihara, T.
FEBS Lett. 336, 317-322, 1993
A;Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) which
A;Reference number: S40454; MUID:94085630; PMID:8262253
A;Accession: S40454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <SAE>
A;Cross-references: UNIPROT:P35413; UNIPARC:UPI0000025C17; GB:D21062; NID:G455487; PIDN:
A;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

Query Match 18.7%; Score 338; DB 2; Length 330;
Best Local Similarity 32.3%; Pred. NO. 3e-20;
Matches 93; Conservative 50; Mismatches 109; Indels 36; Gaps 10;

Qy 38 AFIVILCCA---IVVENLVLIIVARNKSFHSAVYFLGNLAASDLLAGVAFV---ANTL 91
Db 42 AWDVVLICISGLTVSCENALVAIIIVGTPAPAPMFLVGLSLAVADLLAGLGLVLFHFAADF 101
Qy 92 LSGSVTLRLTPVQWFAREGSAFILTASVFSLLATAIERHVAIAKVKLYGSDKS-CRMLL 150
Db 102 CIGSPMSMLV-----GVLMAFTASIGSLLAITVDRIYSLYNALTYSETTTRTYV 155
Qy 151 LIGASWLSVLVGLPIGLWNCGLHLEACSTVLPYAKHYVLCVVTFPSI--ILLAIVAL 208
Db 156 MLALVWVGALGLGVPLVLANCRDGLTTCGVVYPLSKNHLVLAIAFPFMFGIMQLVYAQ 215
Qy 209 YVRIYCVVRSSHADMAAPQTLAL-----LKTVTIVLGVFVLCWLPAPSLILLDY 257
Db 216 ICRIVC-----RHAQOIALQRHLLPASHYVATRKGIATLAVVLGAPACWLPFTVYCLGD 271
Qy 258 ACPVHSCPILYKAHYKFAVSTLNSLLNPVIYTWRSRDLRREVLRPLQC 305
Db 272 A-----DSRLY-TYLTLPATYNSMINPIYAFRQDVQK-VLWAICC 313

RESULT 15
A33117
cannabinoid receptor CB1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A33117; C55879
R;Matsuda, L.A.; Lolait, S.J.; Brownstein, M.J.; Young, A.C.; Bonner, T.I.
Nature 346, 561-564, 1990
A;Title: Structure of a cannabinoid receptor and functional expression of the cloned cDN
A;Reference number: A33117; MUID:90332039; PMID:2165259
A;Accession: A33117
A;Molecule type: mRNA
A;Residues: 1-473 <MAT>
A;Cross-references: UNIPROT:P20272; UNIPARC:UPI000012710C; GB:X55812; NID:G1552375; PIDN:
R;Shire, D.; Carillon, C.; Kaghad, M.; Calandra, B.; Rinaldi-Carmona, M.; Le Fur, G.; Ca
J. Biol. Chem. 270, 3726-3731, 1995
A;Title: An amino-terminal variant of the central cannabinoid receptor resulting from al
A;Reference number: A55879; MUID:95181329; PMID:7876112
A;Accession: C55879
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-107 <SHI>
A;Cross-references: UNIPARC:UPI000017C8D8
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 16.7%; Score 302; DB 2; Length 473;
Best Local Similarity 28.0%; Pred. NO. 3.7e-17;
Matches 92; Conservative 58; Mismatches 129; Indels 50; Gaps 8;

Qy 12 NKQOEYNYTKETLQEQ-----TTSRQVASAFI-VILCCAIWVENLLVIAVA 59
Db 84 NKSLSFPKEENIEICGENFMDMECFMILNPSQQLAIAVLSITLTGTFVLENLLVLCVIL 143
Qy 60 RNSKPH-SAMVYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFILTSA 118

Db 144 HRSRLRCRPSVHFIFGSLAVADLLGSLVIFVSVDFVHFVHRKDSNPVFLFKLGGVTASTFA 203
Qy 119 SVFSLLAIAIERHVAI-----AKVKLYGSDKSCRMILLIGASWLSLVLGGPLPILGWNCGLG 174
Db 204 SVGSLFLTAIDRYFSIHRPLAYKRIVTRPKAVVAFCLM---WTIAIVIAVLPLLLGWNCCK 260
Qy 175 HLEACSTVLPYAKHYVLCVVTFPSIILLAIVALYVRIYCVVRSSHADM----- 223
Db 261 LQSVCSDFPLIDETILMFVIGVTSVLLLFIVYAYMYILWKAHSHAVRMIQRGTQKSI 320
Qy 224 -----AAPQTLALKTVTIVLGVFVLCWLPAPSLILLDYACPVHSCPILYK 269
Db 321 HTSEDKGVQVTRPPQARMDIRLAKTLVLVLVLIICWGPLLAIMVYDFVFGKNK---LIK 377
Qy 270 AHYXFA--VSTLNSLLNPVIYTWRSRDLR 296
Db 378 TVFAFCSMCLLNSTVNPPIIYALRSKDLR 406

Search completed: December 4, 2005, 06:52:57
Job time : 25.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:24:31 ; Search time 130 Seconds
(without alignments)
1193.082 Million cell updates/sec

Title: US-10-084-507B-17
Perfect score: 1806
Sequence: 1 MGSLEYLNPNKQEHYNY.....LERGHMPTPTFLEGNTVW 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq 21:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*
 - 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|------------|--------------------|
| 1 | 1804 | 99.9 | 353 | 2 AAY28288 | Aay28288 Predicted |
| 2 | 1804 | 99.9 | 353 | 2 AAY49904 | Aay49904 Human EDG |
| 3 | 1803 | 99.8 | 353 | 2 AAY28289 | Aay28289 EDG-4 ami |
| 4 | 1787 | 98.9 | 353 | 3 AAB18889 | Aab18889 Amino aci |
| 5 | 1787 | 98.9 | 353 | 6 ABP59285 | Abp59285 Human Edg |
| 6 | 1787 | 98.9 | 353 | 6 ABP59285 | Abp59285 Human Edg |
| 7 | 1787 | 98.9 | 353 | 6 ABP59285 | Abp59285 Human Edg |
| 8 | 1787 | 98.9 | 353 | 6 ABP59285 | Abp59285 Human Edg |
| 9 | 1787 | 98.9 | 353 | 7 ADD11247 | Add11247 Human EDG |
| 10 | 1787 | 98.9 | 353 | 7 ADD11247 | Add11247 Human EDG |
| 11 | 1787 | 98.9 | 353 | 7 ADD11247 | Add11247 Human EDG |
| 12 | 1787 | 98.9 | 353 | 8 ADH57161 | Adh57161 Human end |
| 13 | 1787 | 98.9 | 353 | 8 ADH57161 | Adh57161 Human end |
| 14 | 1787 | 98.9 | 353 | 8 ADH57161 | Adh57161 Human end |
| 15 | 1787 | 98.9 | 353 | 8 ADH57161 | Adh57161 Human end |
| 16 | 1787 | 98.9 | 353 | 8 ADH57161 | Adh57161 Human end |
| 17 | 1787 | 98.9 | 353 | 8 ADH57161 | Adh57161 Human end |
| 18 | 1783 | 98.7 | 353 | 2 AAY49905 | Aay49905 Human EDG |
| 19 | 1783 | 98.7 | 353 | 2 AAY49905 | Aay49905 Human EDG |
| 20 | 1755 | 97.2 | 353 | 9 ADU92079 | Adu92079 Human end |
| 21 | 1631.5 | 90.3 | 352 | 3 AAB03966 | Aab03966 Murine ED |
| 22 | 1625.5 | 90.0 | 352 | 2 AAW01663 | Aaw01663 Fragment |
| 23 | 1625.5 | 90.0 | 352 | 2 AAW01663 | Aaw01663 p(H218). |
| 24 | 1625.5 | 90.0 | 352 | 2 AAY05492 | Aay05492 Human EDG |

| | | | | | |
|----|--------|------|-----|------------|--------------------|
| 25 | 1625.5 | 90.0 | 352 | 2 AAW87790 | Aaw87790 Rat H218, |
| 26 | 1625.5 | 90.0 | 352 | 4 AAU00305 | Aau00305 LPA recep |
| 27 | 1625.5 | 90.0 | 352 | 6 ABU07712 | Abu07712 Rat lysop |
| 28 | 1625.5 | 90.0 | 352 | 6 ABP98696 | Abp98696 Rat Endot |
| 29 | 1625.5 | 90.0 | 352 | 7 ABU61816 | Abu61816 Human sph |
| 30 | 1625.5 | 90.0 | 352 | 8 ADP88361 | Adp88361 Rat endot |
| 31 | 1625.5 | 90.0 | 353 | 7 ADD48927 | Add48927 Rat Prote |
| 32 | 1622.5 | 89.8 | 352 | 6 ABB98695 | Abb98695 Murine En |
| 33 | 1622.5 | 89.8 | 352 | 8 ADO29294 | Ado29294 Mouse GPC |
| 34 | 1509.5 | 83.6 | 377 | 8 ADP29509 | Adp29509 Human sec |
| 35 | 1432 | 79.3 | 372 | 6 ABP59289 | Abp59289 Chimeric |
| 36 | 947 | 52.4 | 269 | 4 ADG15135 | Adg15135 Human 7 t |
| 37 | 947 | 52.4 | 274 | 4 AAM96680 | Aam96680 Human rep |
| 38 | 947 | 52.4 | 274 | 4 ABB96585 | Abb96585 Human tes |
| 39 | 947 | 52.4 | 274 | 4 ADG15162 | Adg15162 Human 7 t |
| 40 | 860.5 | 47.6 | 384 | 6 ABP59281 | Abp59281 Chimeric |
| 41 | 858.5 | 47.5 | 384 | 6 ABP59280 | Abp59280 Chimeric |
| 42 | 858 | 47.5 | 391 | 6 ABP59279 | Abp59279 Chimeric |
| 43 | 854.5 | 47.3 | 362 | 5 ABG75679 | Abg75679 Human Edg |
| 44 | 854.5 | 47.3 | 362 | 8 ADO28787 | Ado28787 Arrestin |
| 45 | 854.5 | 47.3 | 362 | 9 ADX44606 | Adx44606 Chimeric |

ALIGNMENTS

RESULT 1

AAY28288

ID AAY28288 standard; protein; 353 AA.

AC AAY28288;

DT 12-OCT-1999 (first entry)

DE Predicted polypeptide product from human EDG-4 cDNA.

KW EDG-4; polypeptide; receptor; inflammation; amino acid; G protein;
lysolipid; immune response.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 273

FT /label= unknown

FT /note= "encoded by YTT"

PN WO9935259-A1.

PD 15-JUL-1999.

XX 30-DEC-1998; 98WO-CA001195.

PR 30-DEC-1997; 97US-0070185P.

PR 03-APR-1998; 98US-0080610P.

PR 25-NOV-1998; 98US-0109885P.

XX (ALIX) ALLELIX BIOPHARMACEUTICALS INC.

XX Munroe DG, Kamboj R, Peters D, Kooshesh F, Vyas TB, Gupta AK;

XX WPI; 1999-430392/36.

XX New isolated lysolipid/EDG receptor useful in the treatment of asthma and
rheumatoid arthritis.

XX Claim 7; Fig 16A; 120pp; English.

XX A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4) . The LL/EDG
receptors are involved in an inflammatory response signaling pathway and
an apoptotic signaling pathway. They can be used for identifying agonists
or antagonists of NF-kB or IL-8 modulated EDG or LL receptors. Agonists
can be used for upregulation of an inflammatory process condition or
immune response. Antagonists can be used for the downregulation of an

CC inflammatory process condition or immune response. The agonists and
CC antagonists can also be used for controlling apoptosis in a cell
CC comprising the L1/EDG receptor. A diagnostic test for aberrant expression
CC of HEDG-4 can accelerate diagnosis and proper treatment of abnormal
CC conditions of e.g. the heart, kidney, lung and testis. Specific examples
CC of conditions in which aberrant expression of HEDG-4 may play a role
CC include adult respiratory distress, asthma, rheumatoid arthritis, stroke,
CC neurotrauma, Alzheimer's disease, endotoxin shock, atherosclerosis,
CC cardiac ischemia, acute pancreatitis, septic shock, psoriasis, acute
CC cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the
CC liver, and early diabetic glomerulopathy, as well as lung damage
CC following exposure to cigarette smoke, asbestos or silica. HEDG-4
CC specific antibodies, inhibitors, ligands or their analogs can be used as
CC bioactive agents to treat inflammation or disease including viral,
CC bacterial or fungal infections, allergic responses, mechanical injury
CC associated with trauma, hereditary diseases, lymphoma or carcinoma, or
CC other conditions which activate the genes of kidney, lung, heart,
CC lymphoid or tissues of the nervous system

XX Sequence 353 AA;

Query Match 99.9%; Score 1804; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.3e-177;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKVOEHYNYTKETLEQTTSRQVAFIVILCAIIVENLLVLIAR 60
DB 1 MGSLSYELNPNKVOEHYNYTKETLEQTTSRQVAFIVILCAIIVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFVTLASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFVTLASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPIILGNCLGLEACS 180
DB 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPIILGNCLGLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
DB 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPIYKAHYXFAVSTLSLNPVIYVWRSRDLRREV 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPIYKAHYXFAVSTLSLNPVIYVWRSRDLRREV 300
QY 301 RPLQWCPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNVTW 353
DB 301 RPLQWCPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNVTW 353

RESULT 2

AA49904
ID AA49904 standard; protein; 353 AA.

AC AA49904;

DT 28-JAN-2000 (first entry)

DE Human EDG family H218 protein.

KW Human; EDG family; H218; transmembrane receptor protein; diagnosis;
KW therapy; bacterial; fungal; viral; infection; HIV; cancer; diabetes;
KW obesity; anorexia; bulimia; asthma; Parkinson's disease; hypotension;
KW acute heart failure; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; asthma; allergy;
KW benign prostatic hypertrophy; migraine; vomiting; psychotic;
KW neurological disorder; dyskinesia.

OS Homo sapiens.

XX WO9954351-A1.

XX 28-OCT-1999.

XX 14-APR-1999; 99WO-US008099.
PF
XX 23-APR-1998; 98US-0082776P.
PR 03-SEP-1998; 98US-00150650.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Bergsma DJ, Elshourbagy N, Lane P, Li X, Mooney JL, Tsui P;
PI WPI; 1999-633972/54.
XX N-PSDB; AAZ32488.
DR Novel human transmembrane receptor protein for use in treatment and
XX diagnosis of disease.
PT
PS Claim 1; Page 29; 49pp; English.
XX

CC The present sequence is a human EDG family protein designated H218. H218
CC is used for diagnosing disease or its susceptibility in a subject related
CC with expression or activity of H218 by determining the presence or
CC absence of mutation in the polynucleotide encoding H218 in the genome of
CC the subject and/or analysing for the presence of H218 expression in
CC sample derived from the subject. It is also used for treating subjects in
CC need of enhanced activity or inhibition of H218 by administering an
CC agonist or antagonist respectively. H218 can be used to treat abnormal
CC conditions such as bacterial, fungal and viral infections, particularly
CC HIV-1 or 2, cancers, diabetes, obesity, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC stroke, ulcers, asthma, allergies, benign prostatic hypertrophy,
CC migraine, vomiting, psychotic, neurological disorders and dyskinesias can
CC be treated. The H218 polynucleotide can also be used for obtaining
CC hybridisation probes and primers for isolating full-length clones
CC encoding H218. The difference in cDNA or genomic sequence between
CC affected and unaffected individuals is determined to identify mutation
CC causing the disease. It is also valuable for chromosome identification.
CC The polypeptide is used for the identification of membrane bound or
CC soluble receptors through standard receptor binding techniques and also
CC for structure based design of agonist, antagonist or inhibitor of the
CC polypeptides

XX Sequence 353 AA;

Query Match 99.9%; Score 1804; DB 2; Length 353;
Best Local Similarity 99.7%; Pred. No. 1.3e-177;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKVOEHYNYTKETLEQTTSRQVAFIVILCAIIVENLLVLIAR 60
DB 1 MGSLSYELNPNKVOEHYNYTKETLEQTTSRQVAFIVILCAIIVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFVTLASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFVTLASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPIILGNCLGLEACS 180
DB 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPIILGNCLGLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
DB 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPIYKAHYXFAVSTLSLNPVIYVWRSRDLRREV 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPIYKAHYXFAVSTLSLNPVIYVWRSRDLRREV 300
QY 301 RPLQWCPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNVTW 353
DB 301 RPLQWCPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNVTW 353

| | Query Match | 99.8%; | Score 1803; | DB 2; | Length 353; |
|----|-----------------------|--------------------------------------------------------------|---------------------|---------------|------------------|
| | Best Local Similarity | 99.4%; | Pred. No. 1.7e-177; | | |
| | Matches 351; | Conservative | 1; | Mismatches 1; | Indels 0; Gaps 0 |
| Qy | 1 | MGSLYSEYLPNKNKVOEHYNYTKETLTQETTSRQVASAFIVILCCALWENLVLAVAR | 60 | | |
| Db | 1 | MGSLYSEYLPNKNKVOEHYNYTKETLTQETTSRQVASAFIVILCCALWENLVLAVAR | 60 | | |
| Qy | 61 | NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV | 120 | | |

Query Match 98.9%; Score 1787; DB 3; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLYSEYLNPNKQVHEHNYTKETLETQETTSRQVASFIVILCCAIIVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKQVHEHNYTKETLETQETTSRQVASFIVILCCAIIVENLLVLIAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASFITLSASV 120

Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180

Qy 181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTVTV 240
Db 181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTVTV 240

Qy 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQWPRGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLQWPRGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 5
ABP59285
ID ABP59285 standard; protein; 353 AA.
AC ABP59285;
XX
XX
DT 10-MAY-2003 (first entry)
DE Human Edg5 receptor.
KW Human; Edg; receptor.
OS Homo sapiens.
XX
XX WO2003006503-A1.
XX
PD 23-JAN-2003.
XX
PF 10-JUL-2002; 2002WO-US022346.
XX
PR 11-JUL-2001; 2001US-00904099.
XX
PA (CERE-) CERETEK.
XX
PI Shankar G, Munning JN, Spencer JV;
XX
DR WPI; 2003-221718/21.
XX
PT New chimeric Edg receptor, useful in high-throughput screening assays,
PT comprises extracellular and transmembrane domains of a first Edg
PT receptor, and a chimeric intracellular domain of a second Edg receptor.
XX
PS Disclosure; Page 19; 71pp; English.
XX
CC The present invention relates to Edg receptors (ABP59277-ABP59290). The
CC Edg receptors, are useful in a high-throughput screening assay to
CC identify compounds that bind to or modulate the activity of the
CC polypeptide, in calcium mobilisation assays, binding assays, detection of
CC CAMP formation, or in reporter gene techniques
XX
SQ Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 6; Length 353;

Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLYSEYLNPNKQVHEHNYTKETLETQETTSRQVASFIVILCCAIIVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKQVHEHNYTKETLETQETTSRQVASFIVILCCAIIVENLLVLIAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASFITLSASV 120

Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180

Qy 181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTVTV 240
Db 181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTVTV 240

Qy 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQWPRGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLQWPRGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 6
ABB98694
ID ABB98694 standard; protein; 353 AA.
AC ABB98694;
XX
XX
DT 10-JAN-2003 (first entry)
DE Human Endothelial Differentiation Gene, Edg-5.
XX
XX
KW Human; nephrotropic; proliferative glomerular nephritis;
KW Endothelial Differentiation Gene, Edg-5; IGA nephritis.
XX
OS Homo sapiens.
XX
XX WO200277642-A1.
XX
PD 03-OCT-2002.
XX
PF 25-MAR-2002; 2002WO-JP002828.
XX
PR 26-MAR-2001; 2001JP-00088018.
PR 06-SEP-2001; 2001JP-00270551.
XX
PA (NNSH) NIPPON SHINYAKU CO LTD.
XX
XX Takagaki K, Katsuma S, Tsujimoto G;
XX
DR WPI; 2003-018956/01.
DR N-ESDB; ABQ81030.
XX
PT Screening drugs for preventing or treating (mesangial) proliferative
PT glomerular nephritis, based on inhibiting activation of Edg-5 for
PT particularly Edg-5 receptor antagonists.
XX
XX Claim 3; Page 44; 59pp; Japanese.
PS
XX The present invention relates to methods for screening for preventives or
XX remedies for proliferative glomerular nephritis, depending on the
XX inhibitory effect on Endothelial Differentiation Gene, Edg-5, activation.
XX The method is especially useful for screening preventives or remedies for
XX IGA nephritis. The present sequence is human Edg-5, which was used in the
XX method of the invention
SQ Sequence 353 AA;

```
Query Match      98.9%; Score 1787; DB 6; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSEYLNPNKQVQEHYNYTKETLETTQTSRQVASAFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLSYSEYLNPNKQVQEHYNYTKETLETTQTSRQVASAFIVILCCAIIVVENLLVLIAR 60
QY 61 NSKFHSA MYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS AFITLSASV 120
DB 61 NSKFHSA MYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS AFITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRM LLLIGASWLSLVLGGLPILGWNC LGLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRM LLLIGASWLSLVLGGLPILGWNC LGLHLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPI LYKAHYKFAVSTLNSLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPI LYKAHYKFAVSTLNSLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLERGMHMTPTSFLEGN TVV 353
DB 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLERGMHMTPTSFLEGN TVV 353

RESULT 7
ID ABU08813
XX ABU08813 standard; protein; 353 AA.
AC ABU08813;
XX
DT 11-AUG-2003 (first entry)
DE Human EDG-5 protein.
XX
KW Human; lymphocyte activation; lymphocyte migration; EDG-5;
KW G-protein coupled receptor; GPCR; lymphocyte; T cell receptor;
KW B cell receptor; CD69; gene therapy; asthma; allergy; autoimmune disease;
KW multiple sclerosis; scleroderma; pernicious anaemia; IDDM;
KW insulin-dependent diabetes mellitus; tissue transplant;
KW graft-versus-host disease; inflammation; infection.
XX
OS Homo sapiens.
XX
PN US2002155512-A1.
XX
PD 24-OCT-2002.
XX
PF 03-OCT-2001; 2001US-00971228.
XX
PR 18-APR-2001; 2001US-0284763P.
XX
PA (RIGB-) RIGEL PHARM INC.
XX
PI Liao XC, Masuda E, Chu P, Pardo J, Li C, Zhao H, Jiang Y;
XX
XX WPI; 2003-340852/32.
XX
PT Identifying lymphocyte modulator activation/migration, by contacting an
PT EDG G-protein coupled receptor polypeptide or cell having the polypeptide
PT with compound and determining chemical/phenotypic effect of compound on
PT cell.
XX
XX Disclosure; Fig 2; 70pp; English.
XX
XX The invention discloses method for identifying a compound that modulates
CC lymphocyte activation/migration. The method comprises contacting an EDG G
CC -protein coupled receptor (GPCR) family polypeptide, or its fragment or a
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CC cell comprising the polypeptide or its fragment with the compound, and
CC determining the chemical/phenotypic effect of the compound upon the cell.
CC Also disclosed are methods for modulating lymphocyte activation or
CC migration in a subject, by administering to the subject a therapeutically
CC effective amount of an identified compound, an EDG polypeptide or a
CC nucleic acid encoding an EDG, or its fragment, and for screening for
CC modulators of lymphocyte activation, by transfecting into lymphocytes a
CC cDNA library, stimulating T or B cell receptors of the lymphocytes,
CC screening for modulation of lymphocyte activation by detecting the level
CC of CD69 cell surface expression and rescuing cDNAs that modulate
CC lymphocyte activation. The method is useful for identifying a compound
CC (such as an antibody, antisense molecule, small organic molecule,
CC sphingolipid or a sphingolipid analogue) that modulates lymphocyte
CC activation or migration. The compounds identified are useful for the
CC treatment (e.g. gene therapy) of diseases such as asthma, allergy,
CC autoimmune diseases such as multiple sclerosis, scleroderma, pernicious
CC anaemia, insulin-dependent diabetes mellitus, conditions related to organ
CC and tissue transplant such as graft-versus-host disease, acute and
CC chronic inflammation, an infection such as viral, fungal, protozoal or
CC bacterial infections and diseases in which activation of immune response
CC and stimulation of lymphocyte migration is desired. The sequence
CC presented is the human EDG-5 protein
XX
XX Sequence 353 AA;
```

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Query Match      98.9%; Score 1787; DB 6; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 MGSLSYSEYLNPNKQVQEHYNYTKETLETTQTSRQVASAFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLSYSEYLNPNKQVQEHYNYTKETLETTQTSRQVASAFIVILCCAIIVVENLLVLIAR 60
QY 61 NSKFHSA MYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS AFITLSASV 120
DB 61 NSKFHSA MYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS AFITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRM LLLIGASWLSLVLGGLPILGWNC LGLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRM LLLIGASWLSLVLGGLPILGWNC LGLHLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPI LYKAHYKFAVSTLNSLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPI LYKAHYKFAVSTLNSLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLERGMHMTPTSFLEGN TVV 353
DB 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLERGMHMTPTSFLEGN TVV 353
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RESULT 8
ABP82010
ID ABP82010 standard; protein; 353 AA.
XX
XX ABP82010;
AC ABP82010;
XX
XX 04-MAR-2003 (first entry)
DT
DE Human sphingolipid receptor Edg5 protein SEQ ID NO:508.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
```

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.

PN WO200261087-A2.

PD 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; AB242860.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 6; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLPNKQVQEHYNTKETLETTTSRQVASFIVILCCAIWENLLVLIAR 60

DB 1 MGSLSYSLPNKQVQEHYNTKETLETTTSRQVASFIVILCCAIWENLLVLIAR 60

QY 61 NSKFSAMYLFLGNLAASDLLAGAVFANTLLSGSVTLRLTPVQWFAREGSATILSASV 120

DB 61 NSKFSAMYLFLGNLAASDLLAGAVFANTLLSGSVTLRLTPVQWFAREGSATILSASV 120

QY 121 FSLIAIAIERHVAIAKVKLYGSKRCMLLLIGASWLSLVLGGLPIGLWNCGLGLEACS 180

DB 121 FSLIAIAIERHVAIAKVKLYGSKRCMLLLIGASWLSLVLGGLPIGLWNCGLGLEACS 180

QY 181 TVLPLYAKHYVLCVVTTIFSIILALVALVRYICVVRSSHADMAAPQTLALKTTVILG 240

XX |||||

DB 181 TVLPLYAKHYVLCVVTTIFSIILALVALVRYICVVRSSHADMAAPQTLALKTTVILG 240

QY 241 VFIVCWLPAPFISILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRRVL 300

DB 241 VFIVCWLPAPFISILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRRVL 300

QY 301 RPLOCWRPGVCGVGRGRTGPHLLPLRSSSSSLRGHMPETSTFLEGNTVV 353

DB 301 RPLOCWRPGVCGVGRGRTGPHLLPLRSSSSSLRGHMPETSTFLEGNTVV 353

RESULT 9

ADC40485

ID ADC40485 standard; protein; 353 AA.

XX AC ADC40485;

XX 18-DEC-2003 (first entry)

XX Protein of human EDG-5.

DE gene expression analysis; collective quantitative analysis;

KW G protein coupled receptor; tyrosine oxidase receptor family;

KW ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis;

KW myocardial infarction; infarct; ischaemic disease; GPCR; human; EDG-5.

XX Homo sapiens.

OS WO2003052096-A1.

XX 26-JUN-2003.

XX 13-DEC-2002; 2002WO-JP013097.

XX 14-DEC-2001; 2001JP-00382053.

PR 21-FEB-2002; 2002JP-00045104.

PR 15-MAY-2002; 2002JP-00140111.

PR 18-NOV-2002; 2002JP-00333769.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Hinuma S, Kobayashi M, Arai T, Fukusumi S, Fujii R, Komatsu H;

PI Matsumura F, Kawanata Y, Ogi K;

DR WPI; 2003-533023/50.

XX N-PSDB; ADC40486.

PT Method for gene expression analysis for treatment of cancers.

XX Disclosure; SEQ ID NO 46; 261pp; Japanese.

XX The invention relates to a novel method for gene expression analysis by
CC collective quantitative analysis of the expression of a number of genes
CC to identify those that are promoted or inhibited in a given cell or
CC tissue. The genes are preferably gene families such as the G protein
CC coupled receptor family, tyrosine oxidase receptor family, or ion channel
CC gene family. The methods may be used in treatment of cancers, including
CC prostate, ovarian, stomach, bladder, breast, and cancer of the
CC intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used
CC in the treatment and prevention of atherosclerosis, myocardial
CC infarction, infarct or ischaemic disease of the brain. This sequence
CC represents a protein of human EDG-5 of the invention.

XX Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 7; Length 353;

Best Local Similarity 99.2%; Pred. No. 7.5e-176;

Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLPNKQVQEHYNTKETLETTTSRQVASFIVILCCAIWENLLVLIAR 60

DB 1 MGSLSYSLPNKQVQEHYNTKETLETTTSRQVASFIVILCCAIWENLLVLIAR 60

QY 61 NSKFSHMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
DB 61 NSKFSHMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGGPLPILGWNCLGLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGGPLPILGWNCLGLEACS 180
QY 181 TVPLPYAKHYVLCVVTIFSIILALVALYVRIYCVVRSSHADMAAPQTALLKKTIVTIVLG 240
DB 181 TVPLPYAKHYVLCVVTIFSIILALVALYVRIYCVVRSSHADMAAPQTALLKKTIVTIVLG 240
QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMPPTSPFLEGNVTV 353
DB 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMPPTSPFLEGNVTV 353

RESULT 10
ADD11247
ID ADD11247 standard; protein; 353 AA.

XX ADD11247;
XX 01-JAN-2004 (first entry)
XX Human EDG5 protein SEQ ID NO:3.
XX Type II diabetes mellitus; venous thrombosis; pulmonary embolism; EDG5;
KW EDG5 V286A; antidiabetic; thrombolytic; gene therapy; human.
XX Homo sapiens.
XX WO2003085130-A1.
XX 16-OCT-2003.
XX 07-APR-2003; 2003WO-BF003569.
XX 09-APR-2002; 2002EP-00007879.
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX Kozian D, Kostenis E, Siegler K, Jacobs M, Deleuze J, Ricard S;
PI Mace S;
PI WPI: 2003-804314/75.
DR N-PSDB; ADD11248.

XX Identifying an increase in risk for Type II diabetes mellitus and/or
PT venous thrombosis/pulmonary embolism comprises determining in a probe the
PT presence of amino acid exchange at position 286 from Val to Ala in the
PT EDG5 protein.

XX Example 2; SEQ ID NO 3; 21pp; English.

XX The present invention describes a method for identifying an increase in
CC risk for Type II diabetes mellitus and/or venous thrombosis/pulmonary
CC embolism, comprising determining the presence of amino acid exchange at
CC position 286 from Val to Ala in the EDG5 protein. Also described: (1) a
CC method for screening pharmaceuticals useful for treating and/or
CC preventing type II diabetes and/or venous thrombosis/pulmonary embolism,
CC where a cell or cell extract is used that contains EDG5 with the amino
CC acid exchange, or the variation in the nucleotide sequence of EDG5
CC protein or the EDG5-286-AA; (2) a method for adapting the dosage of the
CC pharmaceutical described above by testing the human cell for the presence
CC of EDG5 with the amino acid exchange, or the variation in the nucleotide
CC sequence of EDG5 protein or the EDG5-286-AA; (3) a method of selecting
CC patients who will respond type II diabetes and/or venous
CC thrombosis/pulmonary embolism by testing the probe of the respective

CC patient for the presence of EDG5 with the amino acid exchange, or the
CC variation in the nucleotide sequence of EDG5 protein or the EDG5-286-AA;
CC and (4) a test kit for testing the presence of the amino acid exchange,
CC or the variation in the nucleotide sequence of EDG5 protein or the EDG5-
CC 286-AA. EDG5 has antidiabetic and thrombolytic activities, and can be
CC used in gene therapy. The methods are useful for identifying an increase
CC in risk for type II diabetes mellitus and/or thrombosis/pulmonary
CC embolism, and for screening pharmaceuticals useful for treating type II
CC diabetes mellitus and/or venous thrombosis/pulmonary embolism. The
CC methods are also useful for adapting the dosage of a pharmaceutical
CC useful for treating the above diseases. The methods are useful for
CC selecting patients who will respond to the pharmaceutical. The present
CC sequence represents the human EDG5 protein, which is used in an example
CC from the present invention.

XX Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 7; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSEYLNPNKQEHYNYTKETLTQETTSROVASAFIVILCCAI VVENLLVLIAR 60
DB 1 MGSLSYSEYLNPNKQEHYNYTKETLTQETTSROVASAFIVILCCAI VVENLLVLIAR 60
QY 61 NSKFSHMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
DB 61 NSKFSHMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGGPLPILGWNCLGLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGGPLPILGWNCLGLEACS 180
QY 181 TVPLPYAKHYVLCVVTIFSIILALVALYVRIYCVVRSSHADMAAPQTALLKKTIVTIVLG 240
DB 181 TVPLPYAKHYVLCVVTIFSIILALVALYVRIYCVVRSSHADMAAPQTALLKKTIVTIVLG 240
QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMPPTSPFLEGNVTV 353
DB 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMPPTSPFLEGNVTV 353

RESULT 11
ADD90760
ID ADD90760 standard; protein; 353 AA.

XX ADD90760;
XX 29-JAN-2004 (first entry)
XX Human Edg5 receptor.
KW receptor; human; Edg5 receptor; gastrointestinal disorder;
KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
KW asthma; immune disorder; cognitive disorder; memory disorder; obesity;
KW pain; psychotic behaviour; affective disorder; migraine; cancer; AIDS;
XX wound healing; ischaemia-reperfusion injury-related disease.
XX Homo sapiens.
XX US2003130493-A1.
PN 10-JUL-2003.
XX 26-AUG-2002; 2002US-00228762.
PF 22-FEB-1999; 99US-00253998.
XX 16-JUL-1999; 99US-00356315.
XX

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PA (BONI/) BONINI J A.
PA (HUN/) HUANG L Y.
PA (BORO/) BOROWSKY B E.
PA (SALO/) SALON J A.
PA (WILS/) WILSON A.
PA (NAGO/) NAGORNY R.
XX
XX
XX Bonini JA, Huang LY, Borowsky BE, Salon JA, Wilson A, Nagorny R;
XX WPI; 2003-829581/77.
XX
XX New mammalian Edg7 receptor proteins and nucleic acids encoding mammalian
XX Edg7 receptors, useful for diagnosing and treating an abnormality
XX associated with the activity of the mammalian Edg7 receptor, e.g. asthma,
XX migraine or cancer.
XX
XX Disclosure; SEQ ID NO 19; 64pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a mammalian
XX Edg7 receptor. The mammalian Edg7 receptor proteins and nucleic acid
XX encoding the proteins are useful for diagnosing and treating an
XX abnormality associated with the activity of the mammalian Edg7 receptors,
XX e.g. gastrointestinal disorder, a cardiovascular disorder, hypertension,
XX diabetes, respiratory disorder, asthma, immune disorder, cognitive
XX disorder, memory disorder, obesity, pain, psychotic behaviour, affective
XX disorder, migraine, cancer, AIDS, wound healing, or ischaemia-reperfusion
XX injury-related diseases. The nucleic acids and proteins are also useful
XX for developing and designing drugs with higher specificity and fewer side
XX effects. The nucleic acid probes are useful for detecting nucleic acid
XX encoding mammalian Edg7 receptors and antisense oligonucleotides
XX complementary to the nucleic acid sequences. The methods are also useful
XX for identifying agonists and antagonists of Edg7 receptors. The present
XX sequence represents the amino acid sequence of the human Edg5 receptor.
XX
XX Sequence 353 AA;
XX
XX Query Match 98.9%; Score 1787; DB 7; Length 353;
XX Best Local Similarity 99.2%; Pred. No. 7.5e-176;
XX Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MGSLSYSELYNPNKQEHYNTKETLETTTSRQVASAFIVILCCAIWVENLLVLIAR 60
XX |
XX 1 MGSLSYSELYNPNKQEHYNTKETLETTTSRQVASAFIVILCCAIWVENLLVLIAR 60
XX
XX 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATILSASV 120
XX |
XX 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATILSASV 120
XX
XX 121 FSLAIAIERHVAITAKVLYGSDKSCRMLLIGASWLISLVGLPILGNWCLGLEACS 180
XX |
XX 121 FSLAIAIERHVAITAKVLYGSDKSCRMLLIGASWLISLVGLPILGNWCLGLEACS 180
XX
XX 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
XX |
XX 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
XX
XX 241 VFIWCWLPAPFISILLDYACPVHSCPILYKAHYHFAVSTLNSLLNPVIYTWRSDLRREVL 300
XX |
XX 241 VFIWCWLPAPFISILLDYACPVHSCPILYKAHYHFAVSTLNSLLNPVIYTWRSDLRREVL 300
XX
XX 301 RPLQCRPGVGQGRGRTGPHLLPLRSSSLERGMHMTSPTELEGNTVV 353
XX |
XX 301 RPLQCRPGVGQGRGRTGPHLLPLRSSSLERGMHMTSPTELEGNTVV 353
XX
XX RESULT 12
XX ADH57161
XX ID ADH57161 standard; protein; 353 AA.
XX
XX AC ADH57161;
XX
XX DT 25-MAR-2004 (first entry)
XX
```

```
DE Human endothelial differentiation factor 5 (EDG5) protein SeqID 3.
XX
XX G protein coupled receptor; EDG5; type II diabetes mellitus;
XX venous thrombosis; pulmonary embolism; endothelial differentiation gene;
XX EDG.
XX
XX Homo sapiens.
XX
XX US2003219808-A1.
XX
XX 27-NOV-2003.
XX
XX 21-MAR-2003; 2003US-00393870.
XX
XX 09-AUG-2002; 2002US-0402305P.
XX
XX (KOZI/) KOZIAN D.
XX (KOST/) KOSTENIS E.
XX (SIEG/) SIEGLER K.
XX (JACO/) JACOBS M.
XX (DELE/) DELEUZE J.
XX (RICA/) RICARD S.
XX (MACE/) MACE S.
XX
XX Kozian D, Kostenis E, Sieglér K, Jacobs M, Deleuze J, Ricard S;
XX Mace S;
XX
XX WPI; 2004-060183/06.
XX N-PSDB; ADH57162.
XX
XX Identifying an increase in risk for type II diabetes mellitus, venous
XX thrombosis, pulmonary embolism or its combination in subject by
XX determining whether amino acid residue at position 286 of EDG5 protein is
XX alanine.
XX
XX Example 2.4; SEQ ID NO 3; 10pp; English.
XX
XX This invention relates to a novel method for identifying an increase in
XX risk for type II diabetes mellitus, venous thrombosis, pulmonary embolism
XX or a combination thereof. Specifically, it refers to a the endothelial
XX differentiation gene 5 (EDG5) located on chromosome 19p13.2, which
XX encodes a G protein coupled receptor protein. The present invention
XX describes an immunochemically reactive labelled antibody based kit that
XX can be used to identify the Val286Ala variation in the EDG5 protein
XX encoded by a single nucleotide polymorphism. Furthermore, this allele
XX encoding the V286A variant represents a genetic marker that can be useful
XX for preventative treatments of the aforementioned diseases, as well as
XX for adapting drug dosage for patients, for drug screening purposes or for
XX patient selection in phase or clinical studies. This polypeptide sequence
XX is the human EDG5 protein of the invention.
XX
XX Sequence 353 AA;
XX
XX Query Match 98.9%; Score 1787; DB 8; Length 353;
XX Best Local Similarity 99.2%; Pred. No. 7.5e-176;
XX Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MGSLSYSELYNPNKQEHYNTKETLETTTSRQVASAFIVILCCAIWVENLLVLIAR 60
XX |
XX 1 MGSLSYSELYNPNKQEHYNTKETLETTTSRQVASAFIVILCCAIWVENLLVLIAR 60
XX
XX 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATILSASV 120
XX |
XX 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATILSASV 120
XX
XX 121 FSLAIAIERHVAITAKVLYGSDKSCRMLLIGASWLISLVGLPILGNWCLGLEACS 180
XX |
XX 121 FSLAIAIERHVAITAKVLYGSDKSCRMLLIGASWLISLVGLPILGNWCLGLEACS 180
XX
XX 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
XX |
XX 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
XX
```

QY 241 VFVLCWLPAPFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPIVYTWRSRDLRREVL 300
|||||
DB 241 VFVLCWLPAPFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPIVYTWRSRDLRREVL 300
|||||
QY 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
|||||
DB 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
|||||

RESULT 13

ADJ62652
ID ADJ62652 standard; protein; 353 AA.
XX
AC ADJ62652;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human endothelial differentiation gene 5 protein.
XX
KW Human; receptor; antisense gene therapy;
KW endothelial differentiation gene 5; EDG5; G protein-coupled receptor;
KW development; wound healing; tissue regeneration; cellular proliferation;
KW apoptosis; cancer; angiogenesis; inflammation;
KW hyperproliferative disorder; developmental disorder.
XX
OS Homo sapiens.
XX
FN US2004029274-A1.
XX
PD 12-FEB-2004.
XX
PF 09-AUG-2002; 2002US-00215821.
XX
PR 09-AUG-2002; 2002US-00215821.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Wyatt J;
XX
DR WPI; 2004-179674/17.
DR N-PSDB; ADJ62544.
XX
PT New antisense oligonucleotide targeted to nucleic acid encoding
PT endothelial differentiation sphingolipid G-protein-coupled receptor 5,
PT for treating cancer, developmental disorder or a condition arising from
PT aberrant apoptosis.
XX
PS Disclosure; Page 31-32; 50pp; English.
XX
CC The invention relates to a compound 8-80 nucleobases in length targeted
CC to, and which specifically hybridizes with a nucleic acid molecule
CC encoding endothelial differentiation gene 5 (EDG5, a G protein coupled
CC receptor, involved in development, wound healing, tissue regeneration,
CC cellular proliferation, apoptosis, cancer, angiogenesis and
CC inflammation), and inhibits the expression of EDG5, i.e. is an antisense
CC (AS) oligonucleotide. Also included are a composition comprising the
CC compound and a carrier or diluent and a method for screening an antisense
CC compound (by contacting a preferred target region of a nucleic acid
CC molecule encoding EDG5 with one or more candidate antisense compounds
CC comprising at least an 8-nucleobase portion that is complementary to the
CC preferred target region and selecting for one or more candidate antisense
CC compounds that inhibit the expression of a nucleic acid encoding EDG5).
CC The compound, composition and methods are useful for treating a disease
CC or condition associated with EDG5, such as a hyperproliferative disorder,
CC developmental disorder or a disease or condition arising from aberrant
CC apoptosis. They are also useful in research and diagnostics for
CC modulating the expression of EDG5. Experimental protocols are described
CC but no results are given. The present sequence is the human EDG5 protein.
XX
SQ Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 8; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;

Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGSLYSEYLNPNKQOEYNYTKETLTQETTSROVASAFIVILCCAIVVENLLVLIAR 60
|||||
DB 1 MGSLYSEYLNPNKQOEYNYTKETLTQETTSROVASAFIVILCCAIVVENLLVLIAR 60
|||||
QY 61 NSKFHSAMYLEFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
|||||
DB 61 NSKFHSAMYLEFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
|||||
QY 121 FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
|||||
DB 121 FSLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
|||||
QY 181 TVLPLYAKHYVLCVVTIFSIILALVALYVRIYCVVRSRSHADMAAPOTLALKTTVIVUG 240
|||||
DB 181 TVLPLYAKHYVLCVVTIFSIILALVALYVRIYCVVRSRSHADMAAPOTLALKTTVIVUG 240
|||||
QY 241 VFVLCWLPAPFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPIVYTWRSRDLRREVL 300
|||||
DB 241 VFVLCWLPAPFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPIVYTWRSRDLRREVL 300
|||||
QY 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
|||||
DB 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
|||||

RESULT 14

ADO29293
ID ADO29293 standard; protein; 353 AA.
XX
AC ADO29293;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR EDG5, SEQ ID NO:394.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antisecretory;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
XX
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, Meilwein KL, Pavlova MN, Vassilatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
DR N-PSDB; ADO29865.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying

CC chronic obstructive pulmonary disease. The nucleotide sequences encoding
CC EDG5 are useful as hybridization probes, in constructing oligomers for
CC PCR, for chromosome and gene mapping, in the recombinant production of
CC EDG5, in generating antisense DNA or RNA and in molecular biology
CC techniques that have not yet been developed. EDG5 polypeptides are useful
CC for immunising a mammal to produce polyclonal antibodies and for
CC diagnostic purposes. This sequence represents the human EDG5 receptor
CC protein of the invention.
XX
SQ Sequence 353 AA;

| | | | | |
|-----------------------|-----------------|--------------------------------------------------------------|-----------|-------------|
| Query Match | 98.9%; | Score 1787; | DB 8; | Length 353; |
| Best Local Similarity | 99.2%; | Pred. No. 7.5e-176; | | |
| Matches 350; | Conservative 0; | Mismatches 3; | Indels 0; | Gaps 0; |
| QY | 1 | MGSLYSEYLNPNKQEHYNYTKETLETTQETTSRQVASAFIVILCCAIYVENLLVLIIVAR | 60 | |
| Db | 1 | MGSLYSEYLNPNKQEHYNYTKETLETTQETTSRQVASAFIVILCCAIYVENLLVLIIVAR | 60 | |
| QY | 61 | NSKFHSAMYLPLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV | 120 | |
| Db | 61 | NSKFHSAMYLPLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV | 120 | |
| QY | 121 | FSLLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLLISLVLGGLPILGNCLGLEACS | 180 | |
| Db | 121 | FSLLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLLISLVLGGLPILGNCLGLEACS | 180 | |
| QY | 181 | TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVRRSHADMAAPOTLALKTTIVILG | 240 | |
| Db | 181 | TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVRRSHADMAAPOTLALKTTIVILG | 240 | |
| QY | 241 | VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL | 300 | |
| Db | 241 | VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL | 300 | |
| QY | 301 | RLQCMWRPGVGQGRRRGTPGHLLPLRSSSLERGMHMTPTPTFLEGNTVV | 353 | |
| Db | 301 | RLQCMWRPGVGQGRRRVCTPGHLLPLRSSSLERGMHMTPTPTFLEGNTVV | 353 | |

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